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Title:
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               Score
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length: 2000000000
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Match Length
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1. /ggn2_6/ptodata/2/laa/5A_COMB.pep:*

2. /cgn2_6/ptodata/2/laa/5B_COMB.pep:*

3. /cgn2_6/ptodata/2/laa/6A_COMB.pep:*

4. /cgn2_6/ptodata/2/laa/6B_COMB.pep:*

5. /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodata/2/laa/backfiles1.pep:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-646-265A-132
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Sequence 11, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 9, Appl Sequence 4, Appl Sequence 4, Appl Sequence 19, Appl Sequence 132, Appl Sequence 109, Appl Sequence 10, Appl Sequence 11, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 11, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 16, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 59, Appl Sequence 59, Appl Sequence 59, Appl Sequence 59, Appl Sequence 63, Appl Sequence 63, Appl
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RESULT 1 US-08-561- US-08-561- US-08-561- US-08-561- US-08-561- US-08-561- US-08-561- US-08-561- US-08-561-	00000000000000000000000000000000000000
11, Application US/ 0. 5840299 0. 5840299 0. 5840299 0. 5840299 0. 1840299 1 INFORMATION: CANT: Bendig, Mary CANT: Leger, Olivie CANT: Saldanha, Jos CANT: Jones, S. Tar OF INVENTION: Human OF INVENTION: Human OF INVENTION: Adhe R OF SEQUENCES: 45 SEPONDENCE ADDRESS: SEPONDENCE ADDRESS: RESSEE: Townsend an EET: One Market Pla Y: San Francisco TE: California VI San Francisco TE: California VI SA FREDABLE FORM: UM TYPE: Floppy di PUTER: IBM PC COMPARE: PATON DATA: ICATION NUMBER: US INC DATE: US INC DATE: US-JAN-19 INC DATE: SSIFICATION NUMBER: US INC DATE:	484.5 74.0 135 1 484.5 74.0 139 2 484.5 74.0 139 3 484.5 74.0 139 3 484.5 74.0 139 3 481 73.4 121 3 473 72.2 123 2 473 72.2 123 2 473 72.2 123 2 473 72.2 123 2 473 72.2 123 2 473 72.2 123 2 473 72.2 123 2 473 72.2 123 2 473 72.2 123 3 473 72.2 123 3 473 72.2 123 3 473 72.2 123 3 473 72.2 123 3 473 72.2 123 3 473 72.2 123 3 473 72.2 123 3 473 72.2 123 3
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rew 2000	Sequence 112, App Sequence 119, Appl Sequence 19, Appl Sequence 19, Appl Sequence 23, Appl Sequence 23, Appl Sequence 74, Appl Sequence 53, Appl Sequence 63, Appl Sequence 64, Appl Sequence 66, Appl

Query Match Best Local Similarity

100.0%;

Score 655; DB 2; Pred. No. 1.8e-58;

Length 123;

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GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/186

FILING DATE: 25-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William L.

REGISTRATION NUMBER: 30,223

REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO:
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APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CONDECTON TO THE PROPERTY AND THE PROPERTY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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STRANDEDNESS: single
TOPOLOGY
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                    61 DPKFQGRVTTTADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 123;
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                                                PCT-US95-01219-17
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-561-521-17
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                                                                                                                                                                                                                                           Matches 123; Conservative
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMMBER: US/08/186
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 1527
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Saldanha, APPLICANT: Jones, S.
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140 VSS 142
                                     121 VSS 123
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STATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                        80 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYMGQGTLVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                         20 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 79
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                                                                                                                  61 DPKFQGRYTITADTSASTAYMELSSLRSEDTAYYYCAREGYYGNYGYYAMDYWGQGTLYT 120
                                                                                                                                                                                1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                                                                                                                      100.0%; Score 655; DB 2; Length 142; 100.0%; Pred. No. 2.2e-58; rative 0; Mismatches 0; Indels
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Sequence 17, Application PC/TUS9501219

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                                                                                                                                              Sequence 9, Application US/08561521
Patent No. 5840299
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NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William
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APPLICANT: Jones, S. Tarran
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 142 amino acid
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TELEPHONE: 415-543-9600
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CITY: San Francisco
            APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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REGISTRATION NUMBER: 30
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        140 VSS 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 amino acids
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APPLICATION NUMBER: US/08/186
FILING DATE: 25-JAN-1994
ATTOGNEY_AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
TELLECOMMUNICATION INFORMATION:
TELLEPHONE: 415-543-9600
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INFORMATION FOR SEQ ID NO: 9:
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LENGTH: 123 amino acids
                                                                                                                                                                                          APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
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COMPUTER: IBM PC compatible
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                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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B4.3%; Score 552; DB 2; Length 123;
Local Similarity 82.9%; Pred. No. 3.5e-48;
hes 102; Conservative 11; Mismatches 10; Indels
                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                   121 VSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGYYAMDYWGQGTLVT 120
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                                                                                                          CITY:
                                                                                       STATE:
                                                                                                                          STREET:
                                                                   COUNTRY:
                                                                                                                                             ADDRESSEE:
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One Market Plaza, Steuart Tower, Suite 2000
                                                                                                          San Francisco
                                                                                           California
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                                                                                                                          One Market Plaza, Steuart Tower, Suite
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                                                                         USA
                                                                                                                                           Townsend and Townsend Khourie and Crew
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25-JAN-1994
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US-08-561-521-4
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PRIOR APPLICATION NUMBER: US/08/186,269A
                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9500
                                                                                                                                                                                                                                                                                                                     APPLICANT: Saidanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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                                                                     FILING DATE:
                                                                                                                                                    COMPUTER:
                                                   CLASSIFICATION: 424
                                                                              APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                               STATE:
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PRIOR APPLICATION DATA:
US 08/186,269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 25-JA
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                                                                                                                                                                                                              94105
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amino acid
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                                                                                                                                                                 Floppy disk
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PCT-US95-01219-4
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           TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
                                            APPLICATION NUMBER: US 08/186
FILING DATE: 25-TAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                   SOPTWARE: Patentin Release #1.0, Version #1.25
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
RUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                TELEPHONE: 415 J. TELEPHONE: 415-543-5043
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                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 83.1%; Score 544; DB 2; Length 140; Local Similarity 82.6%; Pred. No. 2.6e-47; hes 100; Conservative 11; Mismatches 10; Indels
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One Market Plaza, Steuart Tower, Suite 2000
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TOPOLOGY:
US-08-871-488A-19
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                                                                                            TELEFAX: (206) 682-60: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION UMBER: US/08/871,488A FILING DATE: 09-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE TITLE OF INVENTION: ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN TITLE OF INVENTION: PRETARGETING METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Sharkey Ph.D., Ric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                           NAME: Sharkey Ph.D., Richard G. REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 690022
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
                                                                                                                                                                                                                            CLASSIFICATION:
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Hylarides, Mark D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reno, John M.
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               linear
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                                                                                                                                (206) 622-4900
                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                          6) 02-6031
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NO: 19:
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82.6%; Pred. No. 2.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scott S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jan T.
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; Patent No. 6214973
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                                                                                                                 ; MOLECULE TYPE: protein US-08-646-265A-132
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Best Local Similarity
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                                 Matches 103; Conservative
                                                                Query Match
                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 132:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 5-
FILING DATE: 19-NOV-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: WO PFILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
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                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
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                                                                                                                                                                                                                       TELEFAX: V= 904136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 09-SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                    TYPE:
                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                LENGTH:
1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                  Local Similarity
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                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                    WEGNER, Harold C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSUCHIYA, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SATO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OHTOMO, Toshihiko
                                                                                                                                                                                                                                                   (202)672-5399
                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                   UMBER: JP 5-291078
19-NOV-1993
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                                                  79.8%;
83.7%;
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                                 Score 523; DB 4; Length 117; pred. No. 2.6e-45; 4; Mismatches 10; Indels
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APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, MASAYUKİ
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: WO POST FILING DATE: 19-OCT-1994 PRIOR APPLICATION DATA:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: WO PCT/JP94/01763
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MEDIUM TYPE: Floppy disk
80 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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TELEFAX: \-
TEX: 904136
                                     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                         20 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 79
                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
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                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                    136 amino acids
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                                                                                                                                                          Conservative
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                               79.8%; Score 523; DB 4; Length 136; 83.7%; Pred. No. 3.1e-45;
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RESULT
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US-08-646-265A-109
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646 >ff
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APPLICANT: OHTOMO, Toshihiko
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ATTORNEY/AGENT INFORMATION:
NAME: WEGNER. Harria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
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APPLICATION NUMBER:
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APPLICANT: SATO, Koh
APPLICANT: TSUGHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
                                                 137 VSS 139
                                                                                  121 VSS 123
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                                                                                                            83 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 136
                                                                                                                                61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                23 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 82
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CITY: Washington
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3000 K Street, N.W., Suite 500
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                                                                                                                                                                                                                                                                     79.8%; Score 523; DB 4; Length 269; 83.7%; Pred. No. 6.9e-45;
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RESULT 14
PCT-US95-01219-13
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: SMILT, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 13:
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                                          APPLICANT:
                                                                APPLICANT:
      TITLE OF INVENTION:
                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 119 amino acids
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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                                                                                                                                                                                                                                                           121 VSS 123
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TYPE: amino actd
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                          61 DPKFQGRYTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGYYAMDYWGQGTLVT 120
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 78.6%; Score 515; DB 2; Length 119; Local Similarity 82.9%; Pred. No. 1.7e-44; cs 102; Conservative 5; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                        : Bendig, Mary M.
: Leger, Olivier J.
: Saldanha, Jose
: Jones, S. Tarran
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Humanized Antibodies Against Leukocyte
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RESULT 15
US-08-561-521-12
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                                                                                                                                                                                                                                                                   Sequence 12,
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Best Local Similarity
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                                                                                                                                                                                                                             GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                      TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08
FILING DATE: 25-JAN-1994
ATTORNEY_AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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LENGTH: 119 amino acids
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MEDIUM TYPE: Floppy
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                           117 VSS 119
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                CITY: San Francisco
STATE: California
COUNTRY: USA
                                              ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
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TOPOLOGY: lir
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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               California
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Leger, Olivier J.
Saldanha, Jose
Jones, S. Tarran
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One Market Plaza, Steuart Tower, Suite 2000
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82.9%;
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Pred. No. 1.7e-44;
5; Mismatches 12; Indels
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COMPUTER RADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: 19 PC COMPATIBLE
CLASSIFICATION NUMBER: 15270-14
PRICE APPLICATION NUMBER: 15270-14
PRICE APPLI
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Minimum DB
Maximum DB
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Maximum Match 1008
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match Length DB
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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RESULT S26330

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A;Title: Antibodies that are specific for a single amino acid interchange in a protein A;Reference number: $26309; MUID:91341421
A;Accession: $26330
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <578>
A;Residues: 1-104 <578>
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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J. Exp. Med. 174, 613-624, 1991
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                                                                                                                                                                                                                                                                                                           Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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A;Cross-references: EMBL:X59173; NID:g52309; PIDN:CAA418B3.1; PID:g1334059 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                    A;Title: Antibodies that are specific for a single amino acid interchange in a protein A;Reference number: S26309; MUID:91341421 A;Accession: S26329
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                                                                                                 A; Molecule type: mRNA
A; Residues: 1-104 <STA>
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J. Exp. Med. 174, 613-624, 1991
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Pred. No. 1.6e-35;
8; Mismatches 7;
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C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S09365
R;Feddersen, R.; van Ness, B.
Nucleic Acids Res. 17, 9797-9809, 1989
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                                                                                                                                                                                C:Superfamily: immunoglobulin V region; immunoglobulin homology C:Keywords: heterotetramer; immunoglobulin fomology <IMM>
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A: Residues: 1-125 <F
                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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A;Reference number: S09365; MUID:90098844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-106 <MEE>
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A;Reference number: A33936; MUID:89282831
A;Accession: C33936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain V region (VM113) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C:Accession: C33936
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Best Local
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₹ 18 DIOMTQSPSSLSASLGGKVTITCKASQDINKYIAWYOHKPGKGPRLLIHYTSTLQPGIPS 77
                       1 DIOMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natl. Acad.
                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGRDYSFSISNLDPEEIATYYCLQYDSLYTFGGGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIOMTOSPSSISASLGGKVTTTCKASQDINKYLAWYQHKPGKGPRLLIHYTSTLQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K.; Johansson, B.; Schulman, J.; Bona, C.; atl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIOMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                              ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;88
                                                                                                               Similarity
                                                                                                                                                                                                                                                           1-125 <FED>
                                                                                            Conservative
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83.0%;
                                                                                                           82.5%;
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                                                                                                           Pred. No.
                                                                                                                            Score 463.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 478; DB 2; Length 106; Pred. No. 1.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 479; DB 2; Length 104;
Pred. No. 9.7e-35;
9; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Mismatches
                                                                                     Mismatches
                                                                                                         5; DB 2;
2.5e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.; Capra, J.D.
                                                                                     10;
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                                                                                                                          Length 125;
                                                                                     Indels
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F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining
F:98-107/Region: framework 4
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                                                                                                                                                                                                                                                            F;35-49/Region: complementarity-determining
F;35-49/Region: framework 2
                                                                                                                                                                                                                                                                                                                                      C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-107 <SHL>
                                                                                                                                                                                                                                                                                                                     F;16-90/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment) C:Species: Mus musculus (house mouse) C:Date: 16-Sep-1992 *sequence_revision 16-Sep-1992 *text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: PL0270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: PL0231; MUID: 90111618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
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C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N. J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A;Reference number: PH0971; MUID:92381444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-97 <TIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000 C;Accession: pH1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 light chain V region (clone 202.54) - mouse (fragment)
C:Species: Mus musculus (house mouse)
                                                               Matches
                                                                                                         Query Match
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                                                                                 Local Similarity
1 DIQMTQSPSSLSASVGDRYTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGNTYFFTISSLQPEDIATYYCLQYDNLWTF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLFTF 97
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                                                                                                                                                                                                                                                                                                                  immunoglobulin homology <IMM>
                                                        Conservative
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                                                                       79.4%; Score 446.5; DB 2 79.4%; Pred. No. 6.4e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.4%;
                                                   11; Mismatches
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Pred. No. 1.9e-32;
                                                                                               DB 2; Length 107;
                                                 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 97
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61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106

1 DIQMTQSPCSLSASLGDKVTITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

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A:Molecule type: mRNA
A:Residues: 1-129 <ROC;
A:Residues: 1-129 <ROC;
A:Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                            Ig kappa chain V region - human (fragment)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 19-May-1995 *sequence_revision 21-Jul-1995 *text_change 21-Jan-2000
C.Accession: S52789
R.ROCCB, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995
A.Description: Light chain V region gene usage restriction and peculiarities in myeloma-A.Reference number: S52789
A.Reference number: S52789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-90/Domain: immunoglobulin homology 
F:23-88/Disulfide bonds: *status experimental
                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
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A:Contents: annotation; X-ray crystallography, 2.0 angstroms
C:Comment: This is a Bence Jones protein.
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A:Residues: 1-108 <PAL>
A:Residues: 1-108 <PAL>
A:Rosidues: 1-108 <PAL>
A:Rote: the C region of this chain has the Inv (1,2) marker
R:Epp. O.; Lattman, E.E.; Schlifer, M.; Huber, R.; Palm, W.
Biochemistry 14, 4943-4952, 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB: IGKV1
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A:Title: Die Primaerstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom vollstaendige Aminosaeuresequenz des Proteins.
A:Reference number: A91663; MUID:76023758
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C:Date: 24-Apr-1984 #Sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A91663; A01873
R:Palm, W.; Hilschmann, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A: Accession: A91663
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 78.9%; Score 443.5; DB 2 Similarity 79.4%; Pred. No. 1.4e-31;
            Conservative
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81.1%;
      10;
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      Mismatches
                                                          DB 2;
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      Indels
                                                          Length 129;
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F:50-56/Region: complementarity-determining F:57-88/Region: framework 3 F:89-97/Region: complementarity-determining
                                                                                                        F;24-34/Region:
F;35-49/Region:
                                                                                                                                                                                    C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-23/Region: framework 1
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A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain V region (anti-DNA, 6BBVK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0272
F;98-107/Region:
                                                                                                                                                        F;16-90/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-103 <ST2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X59187; NID:g52318; PIDN:CAA41897.1; PID:g1334064 A:Note: the sequence of residues 1-8 and the corresponding nucleic acid se A;Accession: $26331
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A; Residues: 1-103 <STA>
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R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
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N:Alternate names: Ig kappa chain V region
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Best Local Similarity
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                                                                                                          framework 2
                                                                                                                           complementarity-determining
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A; Accession: PLO269
A; Accession: PLO269
A; Accession: PLO269
A; Molecule type: mRNA
A; Residues: 1-107 <SHL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 1-23/Region: framework 1
F; 16-90/Domain: immunoglobulin homology <IMM>
F; 24-34/Region: complementarity-determining 1
F; 35-49/Region: complementarity-determining 2
F; 57-89/Region: framework 3
F; 89-97/Region: complementarity-determining 3
F; 89-97/Region: complementarity-determining 3
F; 98-107/Region: framework 4
                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0269
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PL0231; MUID:90111618
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A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, A;Reference number: A33730; MUID:89367325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain V region (9.42) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 *sequence_revision 18-Sep-1992 *text_change 21-Jan-2000
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A; Residues: 1-94 <LAW>
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Local Similarity 86.2%;
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Pred. No. 2e-31;
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Query Match

Score 439.5;

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A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V region (anti-DNA, 2E3VK) - mouse (fragment)
C;Speciles: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
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F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining
F;89-97/Region: framework 4
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A; Residues: 1-107 <SHI
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A;Accession: PL0271
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                                                                                                                        A;Molecule type: protein A;Residues: 1-108 <SCH>
A;Residues: 1-108 <SCH>
A;Residues: 1-108 <SCH
A;Note: the C region of this chain has the Inv (3) marker
R;Fehlhammer, H.; Schiffer, M.; Epp. O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; S Biophys. Struct. Mech. 1, 139-146, 1975
Biophys. Struct. Mech. 1, 139-146, 1975
A;Title: The structure determination of the variable portion of the Bence-Jones prote A;Title: The structure determination of the variable portion of the Bence-Jones prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;24-34/Region:
F;35-49/Region:
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A; Title: Chemical modification of the carboxyl groups of protein substrates enhances
                       R;Steiner, V.; Chang, J.Y. FEBS Lett. 222, 6-10, 1987
                                                                      A; Note: the structure of the V region was determined by molecular replacement methods
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Local Similarity 78.5%;
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10; Mismatches 12;
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Pred. No. 2.6e-31;
0; Mismatches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Status: preliminary: translated from GB/EMBL/DDBJ A:Molecule type: mRNA A:Residues: 1-108 <RES-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain (BRE) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C;Accession: 139154
R;Schormann, N.; Murrell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A;Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed A; Recession: 139154; MUID:96003804
A;Accession: 139154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an Immunoglobulin heterotetramer subunit consists of two identical light (Kap hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Comain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted
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A:Contents: annotation
C:Comment: This is a Bence Jones protein.
C:Genetics:
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                                                                                                                                          61 RFSGSGSGRDYTFTISSLOPEDIATYYCLOYDNL-WTPGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                / Match 77.5%; Score 435.5; DB 2; Length 108; Local Similarity 79.4%; Pred. No. 5.7e-31; Les 85; Conservative 9; Mismatches 12; Indels 1;
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Title: Perfect score: Sequence:

US-09-010-377-1
562
1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	HC. Bence-Jones protein; 3D-structure. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2. COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3. COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.	SEQUENCE. SEQUENCE. SEQUENCE. MEDILINE-76023758; PubMed-809329; Palm W., Hilschmann N.; Rappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation of the protein; a contribution to the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site."; Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975). [2] Y. RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS). MEDLINE-76039968; PubMed-1182131; MEDLINE-76039968; PubMed-1182131; MEDLINE-76039968; PubMed-1182131; Palm W.;	Created) Created) Last sequence update) Last annotation update) jion Rei. hordata; Craniata; Vertebrata; Euteleostomi; rimates; Catarrhini; Hominidae; Homo.

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Biophys. Struct. Mech. 1:139-146(1975).

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-i. MISCELLANEOUS: THE C REGION OF THIS CHAIN CHAIN SCELLANEOUS: THE S A BENCE-JONES PROTEIN MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN CONTRACTOR OF THE CHAIN CH
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15 kappa chain V-I region AU.
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                                                       COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
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21-JUL-1986 (Rel. (
15-JUL-1999 (Rel. )
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Scand. J. Immunol. 5:677-684(1976).
Scand. J. Immunol. 5:677-684(1976).
-i- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPHO DEFERMINANTS.
WITH WHICH IT SHARES CERTAIN IDIOTYPHO DEFERMINANTS.
                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                      Capra J.D., Klapper D.G.; "Complete amino acid sequence of the variable of IgM anti-gamma globulins (Lay/Pom) with shared
                                                                                                                        SEQUENCE
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
                     DIQMTQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS
                                 DIQMIQSPSSLSASVGDRVTIICKISQDINKYMAWYQQTPGKAPRLLIHYISALQPGIPS
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                                                                 Score 421.5; DB 1
Pred. No. 1.2e-37;
1; Mismatches 13
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8; Mismatches
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Pred. No. 1.
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BY SIMILARIT
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BY SIMILARITY.
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InterPro: IPR00396; 1g_V.
Pfum: PP60047; 1g; 1
SMART: SM00406; IGv: 1
Inmunoglobulin V region; B
DOMAIN 24 34
DOMAIN 35 49
DOMAIN 50 56
DOMAIN 57 88
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
19 kappa chain V-I region Roy.
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"The amino acid sequence of a kappa type Bence-Jones protein, complete sequence and the location of the disulfide bridges.";
J. Blol. Chem. 244:3550-3560(1969),
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3)
                                                                                     Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                   NAMOH
  Hilschmann
                        MEDLINE-68362076; PubMed-5595110.
                                                 SEQUENCE
                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                             Homo sapiens (Human)
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Mammalia; Eutheria; Primates; Catarrhini;
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15-JUL-1999 (Rel. 38, Last an
Ig kappa chain V-I region AG.
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P01593;
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38, Last annotation update)
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                                                                                                                Primates; Catarrhini; Hominidae; Homo
                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 2e-37;
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COMPLEMENTARITY-DETERMINING-3
FRAMEWORK-4.
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COMPLEMENTARITY-DETERMINING-2
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HCHAN

KY1Y_HUMAN

STANDARD;

PRT;

108 AA.

P80362;

01-NOV-1995 (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)
Popp R.A., Solomon A., "Characterization and preliminary crystallographic data on "Characterization" of the human kI Bence Jones protein wat."
                                                                                                                 Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz Solomon A., Stevens F.J., Schiffer M.; "Comparison of crystal structures of two homologous proteins: structural origin of altered domain interactions in immunogloblight-chain dimers.";
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SEQUENCE
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOMAIN
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InterPro; IPR003596; Ig_v.
Pfam; pF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hilschmann N., Barnikol H.U., Hess M., Steinmetz-Kayne M., Suter L., Watanabe (In) Franek F., Shugar D. (eds.);
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                                                 MEDLINE=81267384; PubMed=6167731; Stevens F.J., Westholm F.A., Panagiotopoulos N.,
                                                                                                                                                                                  SEQUENCE, AND x-RAY CRYSTALLOGRAPHY (1.9 MEDLINE=95086080; PubMed=7993911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gamma globulins: structure and function, pp.57-74, New York (1969).
                                                                                                      Biochemistry 33:14848-14857(1994).
                                                                                                                                                                                                                         NCBI_TaxID=9606;
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[2]
                                                                              SEQUENCE OF 1-35.
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Pred. No. 2e-37
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Best Local :
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SMART; SM00406; IGV; IdPuil
                                                                                                                                                                                                                                                                                                                     KV1Q_HUMAN STANDARD; PRT; 108 AA P01609; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation updat 19 kappa chain V-I region Scw.
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SEQUENCE
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Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
                                                                                                                                             PIR; A01875; K1HUSW.
HSSP; P01607; 1REI.
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SMART; SM00406; IGv; 1.
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COMPLEMENTARITY - DETERMINING - 3.
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355:842-866(1974).
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Best Local
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InterPro; IPR003596; Ig_v.
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Klobeck H.G., Combriato G., Zacha
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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13-AUG-1987 (Rel.
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Pred. No. 2.7e-36;
0; Mismatches 16
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Pred. No. 8.4e-37;
                                                                                                                                                                                                                   IG KAPPA CHAIN V-I REGION WALKER FRAMEWORK-1.
                                                                                                                                   BY SIMILARITY
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   REAL REPORT OF THE REAL REPORT O
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Best Local
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interroller (1987) 1.

Pfam; PF00047; 1g; 1.

SMART; SM00406; IGv; 1.

Immunoglobulin V region; Glycoprotein.

Immunoglobulin V region; Glycoprotein.

28 N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KV1D_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *Primary structure of kappa light chain from a human myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-75075135; PubMed-4216454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P01596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - 1 - MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR003006: Ig_MHC.
InterPro: IPR003596: Ig_v.
                        Conl F., Frangione B.;
*Amino acid sequence of the Fv region of a human monoclonal protein wEA) with antibody activity against 3.4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33.";
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 RFSGSGSGTDFTLTISSLQPEDSATYYCQQSYSTLITFGQGTRLEIK 129
                                                                                                                                             MEDLINE-83273707; PubMed-6410398;
                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V-I region WEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KV1R_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTDFTLT1SSLZPBBFATYYCQQYNTFFTFGPGTKVDIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HFSGSGSGRDYTFTISSLOPEDIATYYCLO-YDNLWTFGOGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P80362; 1WTL
   Natl. Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 AA; 11703 MW;
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Sci. U.S.A. 80:4837-4841(1983).
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                            of a human monoclonal IgM
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RESULT
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Best Local :
                                                                                                                                                       SMART; SM00406; IGV;
Immunoglobulin V reg
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A01876; K1HUWE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P80362; 1WTL
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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-i- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
                                                                                                                                                                                                                                                                                                                                                                                           subgroups."
                                                                                                                                                                                                                                                                                                                                                                                                               chain of subgroup I (Bence-Jones Protein Hau):
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe S., Hilschmann N.;
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                                                                                                       DOMAIN
                                                                                                                          DOMAIN
                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                          HSSP; P80362; 1WTL
                                                                                                                                                                                                                                                                                                                                -!- MISCELLANEOUS: THIS IS
                                                                                                                                                                                                                                                                                                                                                                                                                                The primary structure of a monoclonal kappa-type immunoglobulin L-
NON_TER
                     DISULFID
                                         DOMAIN
                                                             DOMAIN
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InterPro; IPR003596; Ig_v
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                                                                                                                                                                                                                                                                                                            A01868; K1HUHU.
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1 23 FRAMEWORK-1.

24 34 COMPLEMENTARITY-DE
25 56 FRAMEWORK-2.

50 56 COMPLEMENTARITY-DE
57 88 FRAMEWORK-3.

68 97 COMPLEMENTARITY-DE
69 107 FRAMEWORK-4.

23 88 BY SIMILARITY.
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IGv; 1.
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                                                                                                                                                                                          Bence-Jones protein
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                                                                                                                                                                                                                                                                                                                                    A BENCE-JONES PROTEIN.
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Pred. No. 2.8
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                                                                    COMPLEMENTARITY-DETERMINING-3
                                                                                                         COMPLEMENTARITY-DETERMINING-2
                                                                                                                                 FRAMEWORK - 2
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                                              FRAMEWORK-4
                                                                                     FRAMEWORK-3
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                                                                                                                           Query Match
                                                                                                                                                                                      InterPro: IPR003596; Ig-V
Pfam; PF00047; ig: 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
DOMAIN 24 34
DOMAIN 35 49
DOMAIN 35 49
DOMAIN 57 88
DOMAIN 57 88
DOMAIN 89 97
DOMAIN 89 97
DOMAIN 89 107
DOMAIN 98 107
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                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
                                                                                                                                                                                                                                                                                                                                                                              PIR; A01866; K1HUEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFIDE BOND.
MEDLINE=71064027; PubMed=4923144;
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                                                                                                                                                                                                                                                                                                                                                                    HSSP; P01607; 1REI
                                                                                                                                                                                                                                                                                                                                                                                     -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gall W.E., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gottlieb P.D., Cunningham B.A., Rutishaus "The covalent structure of a human gamma acid sequence of the light chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     "The covalent structure of a human gamma G-immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 9:3155-3161(1970).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last_annotation update)
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=71064023; PubMed=5489770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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P01598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYD-NLWTFGQGTKVEIK 106
                                                                                                              Local
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                                                            DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                   DIQMTQSPSTLSASVGDRVTITCRASQSINTWLAWYQQKPGKAPKLLMYKASSLESGVPS 60
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLSWYQQKPGKAPQVLIYAASSLPSGVPS 60
                                                                                                            Similarity
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                                                                                                                                                               11788 MW;
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70.1%;
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72.9%;
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                                                                                                       Score 397.5; DB Pred. No. 4e-35;
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                                                                                                                                                                                                                                FRAMEWORK - 3
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Pred. No. 1.2e-35;
                                                                                                                                                          9CD294F2F4D88823 CRC64;
                                                                                             Mismatches
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man gamma G-immunoglobulin. VI. Amino
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immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
J. Biochem. 77:1277-1296(1975).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
                                                                                                                                                               P01603;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                              Shinoda T.
                                        "Comparative structural studies on the light chains of human
                                                                     MEDLINE=76189985; PubMed=818073;
                                                                                      SEQUENCE
                                                                                                            NCBI_TaxID=9606;
                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                    Homo sapiens (Human)
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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13-AUG-1987 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
MOL. Immunol. 23:73-78(1986).
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                                                                                                                                                                                                                                                                                                           61 RFSGSGSGRDYTFTISSLOPEDIATYYCLQYDNL-WTFGOGTKVEIK 106
                                                                                                                                                                                                                                                                                             61 NFTGSGSGTDFILTISSLQPEDFATYYCQQYNSYPYTFGQGTKVQIK 107
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mes 75; Conserv
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Best Local Similarity
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region DEE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The amino acid sequence of a human kappa light chain.";
Blochem. J. 123:945-958(1971).
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InterPro: IPR003596; Ig_v
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                             11661 MW;
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Score 388.5; DB 1; Length 108; Pred. No. 3.6e-34;
                                                                                                                                                                                                             COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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Pred. No. 2.2e-34;
9; Mismatches 16;
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                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-2
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                      BDD6E350017F1E51 CRC64;
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Search completed: July 9, 2002, 15:45:57 Job time: 373 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

Query M Best Lo Matches		RA YOU RATE THE TEST OF THE TE			UL7
Query Match 76.2%; Score 428.5; DB 4; Length 108; Best Local Similarity 76.6%; Pred. No. 1.1e-40; Matches 82; Conservative 8; Mismatches 16; Indels 1; Gaps 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60 1	EMBL; AF035037; AAD56273.1; . HSSP; P01607; 1REI. InterPro; IPR003006; 19_MHC. InterPro; IPR003596; 19_V. Pfam; PF00047; ig; 1. SMART; SM00406; IGV; 1. NON_TER 1 1 1 NON_TER 108 AA; 11738 MW; C06681716C4D16F3 CRC64;	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934; MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; Young D.C.; "Myosin reactive autoantibodies in rheumatic carditis and normal "Myosin reactive autoantibodies in rheumatic carditis and normal fetus.";	(FRAUMENT). HOMO Sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID-9606;	01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION	7 7 Q9UL77 PRELIMINARY; PRT; 108 AA.

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0921A6;
091a6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT)
Mus musculus (Mouse).
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EMBL: U88067; AAB48044.1; -.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
aNTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                          rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
antibody V region genes.";
J. Immunol. 16::2020-2031(1998).
                                                                                                                                                                                                                                                                                        MEDLINE=98375893; PubMed=9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
"Molecular analysis of polyreactive monoclonal antibodies from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIABLE REGION (FRAGMENT).
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates;
        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134
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                                                                                                                         U96396; AAB68785.1;
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241 AA;
        107
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            AA;
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73.68;
        11520 MW;
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Pred. No. 4.5e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
            4BB43E9C5B577F16 CRC64;
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RESULT
Q9UL70
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01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                    Q9UL81 PRELIMINARY; PRT; 107 AA.

Q9UL81;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clin. Immunol. Immunopathol. EMBL; AF035044; AAD56280.1;
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                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Young D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wu X., Liu B., Van der Merwe P.L., Kalis N.N.,
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SEQUENCE FROM N.A.
                                               NCBI_TaxID=9606;
                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                               MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
                                                                                                                                                       (FRAGMENT)
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                                                                            Primates; Catarrhini;
                                                                                                       Chordata;
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75.5%;
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Pred. No. 4.8e-39;
9; Mismatches 17
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Pred. No. 3.4e-38;
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                                                                                                    Craniata; Vertebrata; Euteleostomi;
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                                                                               Hominidae;
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InterPro; IPR003596; Ig-
Pfam; PF00047; Ig; 1,
SMART; SM00406; IGV; 1.
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HSSP; P01607; 1REI
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                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
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Q9UL79;
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                                                                                                                                                                                                                                                                                 fetus."
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SMART; SM00406; IGv; 1.
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RFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFPPTFGQGTKVEIK 107
                                             DIVMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAASTLQSGVPS
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77; Conserv
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                                                                                                         68.6%;
72.0%;
                                                                                                                                                                                                                19_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11501 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.38;
71.78;
                                                                                                                                                                                                                              Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                            Score 385.5; | Pred. No. 7.9e | 8; Mismatches
                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 395; DB 4; Length 107; Pred. No. 6.7e-37;
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                                                                                                                                                       DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108
                                                                                           nes 21;
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                                                                                                                  DB 4; Length 108;
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Query Match
Best Local Similarity
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                         091WS9 PRELIMINARY; PRT; 233 / 091WS9; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence 01-DEC-2001 (TrEMBLrel. 19, Last annotation of the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9R1A5;
                                                                                                                             Hypothetical protein.
                                                                                                                                                                         Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC013496; AAH13496.1; -
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single chain antibody (scFV)."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF152371; AAD40242.1; -. HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust me antibody (Mab 7, its light and heavy chains) and construction single chain antibody (scFV).";
                                                                                                          SEQUENCE
                                                                                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                                                                                                TISSUE-COLON;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00290; IG_MHC; UNKNOWN_1.
NON_TER 1 1
NON_TER 214 214
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SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-DEC-2001 (TYEMBLRel. 19, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                       233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 AA;
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                                                                                                       25781
  67.5%;
69.2%;
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                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Score 379.5; DB 1 Pred. No. 9.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 384.5; DB 1
Pred. No. 2.3e-35;
                                                                                                     B1C184DA149A16EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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SEQUENCE FROM N.A.
MEDLINE=21361171; PubMed=11468171;
MEDLINE=21361171; PubMed=11468171;
Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
The tropism of organ involvement in primary systemic amyloidosis:
The tropism of organ involvement in primary systemic amyloidosis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      096PF6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q96PF6
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                     streptococcal polysaccharide, N-acetyl-glucosamine, with cardiac myosin,";
                                                                            MEDLINE=20448942; PubMed-10992488; Malkiel S., Liao L., Cunningham M.W., Diamond B.; "T-Cell-dependent antibody response to the dominant
                                                                                                                                                        STRAIN-BALB/C;
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     NCBI_FaxID=10090;
                                                                                                                                                                                                                                                                                                                                            (FRAGMENT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIQMTQTTSSLSASLGDRVTISCSGSQGIANYLNWYQQKPDGTVKLLIYYTSSLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFSGGGSATNFTVTISSLQPEDFATYYCQQYHHLPFTFGPGTKVDFK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIQMTQSPSSLSASVGDRVTFICQASQDIANHLNWYQKKPGEAPKFLIYDGSFLKTGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFSGSGSGTDYSLTISNLEPEDIATYYCQQYRYLPWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ar361758; AAK51465.1; -.
ER 1 1
ER 116 116
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Immun. 68:5803-5808(2000),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                Sciurognathi;
                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                   Muridae;
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                                                         cross-reactive
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InterPro; IPR003006; Ig_MH
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 25.9 KDA PROTEIN.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                      O920E6 PRELIMINARY; PRT; O920E6; O1-DEC-2001 (TrEMBLrel. 19, Created) O1-DEC-2001 (TrEMBLrel. 19, Last seq O1-DEC-2001 (TrEMBLrel. 19, Last annumber of the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC015292; AAH15292.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
                                NCBI_TaxID=10090;
                                                              Mammalia; Eutheria; Rodentia;
                                                                                                                                           (FRAGMENT).
                                                                                                                                                                   PTERIN-MIMICKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLYLGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFSGSGSGXDYSLTISNLEPEDIATYYCQQYSKFPWTFGGGTKLEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                    RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTPPFTFGSGTKLEVK
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107 AA;
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                                                                                                                                                                MBLrel. 19, Last sequence update)
MBLrel. 19, Last annotation update)
ANTI-IDIOTOPE KAPPA CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25929 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.3%; Score 355.5; DB 1 64.5%; Pred. No. 4.7e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
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                                                              Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B0D0B0E6EB7812D2 CRC64;
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                                                                    Muridae;
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Best Local :
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InterPro; IPR003006; Ig_MHC
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGV; 2.
O9UL83 PRELIMINARY; PRT;
O9UL83;
O1-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  Shinohara N., Demura T., Fukuda H.; solation of a vascular cell wall-specific monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-BALB/C; TIS
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                method."
                                                                                                                                                                                                                                                                                                                                                                                                                   recognizing a cell polarity by using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/C; TISSUE-SPLEEN; MEDLINE-20183931; PubMed-10706631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AF307938; AAL09422.1; -.
                                                                                                 233 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK 279
                                                                                                                                                        173 DIEUTOSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGVPS 232
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                                                                                                                            61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
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                                                                                                                                                                                                                                       Local
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AB036341; BAA88633.1; -.
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                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                               298 AA;
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                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                TGV; 2.
AA: 31867 MW;
                                                                                                                                                                                                                                 60.1%; Score 337.5; DB 11; Length 58.9%; Pred. No. 6.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.9%;
61.7%;
                                                                                                                                                                                                                                                                                                                                                   IG_MHC
                                                                                                                                                                                                                        19,
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                                                                                                                                                                                                                                                                                         E0F96B8A17004317 CRC64;
                                                                                                                                                                                                                     Mismatches
                               108 AA
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Best Local Similarity
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Q9UL85;
Q9UL85;
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-DEC-2001 (TrEMBLrel. 19,
                                      Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                            InterPro; IPR003596; Ig_v.
                                                                                                                                                            MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
      SEQUENCE
                                                                                          HSSP; P80362;
                                                                                                      EMBL; AF035029;
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                            MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE
                                                                          InterPro; IPR003006; Ig_MHC.
                                                                                                                                fetus."
                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                     Young D.C.
                                                                                                                                                                                                                 NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                      (FRAGMENT)
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-98277139; PubMed-9614934;

Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P80362; 1WTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF035031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNN-WPFTFGPGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                            RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
                                                                                                               Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunol. Immunopathol. 87:184-192(1998).
   109 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                          1WTL.
                                                                                                      AAD56265.1;
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   11761 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Mismatches
                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                   Created)
FB1E43E7C7AFACCC CRC64;
                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                            109 AA
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N

Query Match

59.18;

Score 332;

DB 4;

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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT: *
5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT: *
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Copyright (c) 1993 - 2000 Comp
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                                                                                                                      Mouse anti-VLA-4 a
Mouse VLA-4 antibo
Human VLA-4 reshap
Alpha-4 integrin m
                                                                                                                                                                                                                                                                                                                                                                            Description
                             Human MCP-3 and mu
Human IP-10 and mu
Artificial synthet
                                                                                                                                                                                                                                                         Humanised alpha-4
                                                                                                                                                                                                                                                                                       Humanised
                                                                                                                                                                                                                                                                                                                 Humanized anti-VLA
                                                                                               MCP-3
                                                                                                                                                                                                                                                                                alpha-4
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Single chain Fv pr	AAY55075	21	260	79.1		-
Interleukin-6 s		21	256	79.1	444.5	
pUC-RVh-PMla.	AAR29013	13	126	79.1	444.5	
puc-RV1-PMla.	AAR29015	13	126	79.1	444.5	
Human consensus	AAY82345	21	108	79.1	444.5	
Human consensus fr	AAW70622	19	108	79.1	444.5	_
Human variable lig	AAB61585	22	107	79.1	444.5	
Consensus human	AAB60400	22	107	79.1	444.5	
Human V1 consens	AAB62087	22	107	79.1	444.5	
	AAW87455	20	107	79.1	444.5	
Humanised	AAW70623	19	107	79.3	445.5	
Variable Light o	AAW86804	19	107	79.3	445.5	
Protein encoded	AAW70703	19	237	79.4	446.5	
TF8-5G9 CDR-graf	AAW10233	18	234	79.4	446.5	
Anti-VEG	AAW70673	19	110	79.4	446.5	
CDR-grafte	AAW10231	18	108	79.4	446.5	
Humanised	AAW70625	19	107	•	449.5	
Variable !	AAW86805	19	107	•	449.5	
R. pipien	AAW35133	18	355	80.2	451	
Human/murin	AAR47207	15	129	•	451.5	
Human REI mon	AAR65163	16	108	80.3	451.5	
FWP51 fusion p	AAR26981	13	241		452	
Murine	AAR13658	12	109	80.6	453	
Humanised alph	AAW22422	18	107		453.5	
Humanized	AAR81322	16	107		453.5	
	AAW26800	19	245		455	
Amino acid sec	AAY21882	20	241		455	
	AAR85495	16	240	•	455	
Anti-gp54 MAb	AAW26797	19	109	81.1	456	
(FRP51)-ETA f	AAR26983	13	637	81.9	460	
Variable reg	AAR06252	11	128	•	460.5	
Murine monoclona	AAR93159	17	108	•	465	
varia	68	16	107	83.9	471.5	
CD4-specific CDR-g	AAR13050	12	234	84.6	475.5	

ALIGNMENTS

RESULT AAR81321 antibody engineering. 02-APR-1996 AAR81321; AAR81321 standard; Protein; 106 AA Н (first entry)

Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.

Chimeric Mus musculus Chimeric Homo sapiens

W09519790-A1.

27-JUL-1995.

25-JAN-1995; 95WO-US01219

25-JAN-1994; 94US-0186269

(ATHE-) ATHENA NEUROSCIENCES INC

Bendig MM, Jones TS, Leger OJ, Saldanha

WPI; 1995-269276/35.

inflammatory disease New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating

ME1-14 light

chain

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RESULT
AAW22412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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Best Local
Misc-difference 49
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                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asthma: atherosclerosis: AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia;
                                                                                                                                                                                                                                                                         Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised alpha-4 integrin antibody 21.6 VL La.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67; 105pp; English.
                                                                                                                                                                                                                                                                         /label= CDR1
/note= "21.6
35..49
                                                                                                                                                        /note=
45
                                                                                                                                                                                                                                                                                                                                                                                         /note=
24..34
                                                                                                            /note= "REI Lys-45 is substd. by Lys of mouse
                                                                                                                                                            /label= FR2
/note= "REI framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                              "REI framework region 1"
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                                    loop*
                                                                                                                                                                                                                                                                                                     complementarity determining region 1"
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Pred. No. le-36;
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                                                                        important in supporting the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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21.6 and a modified human REI framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate fragments of mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the manufacture of a medicament for treating asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metastrasis, nephritis, atopic dermatitis, provincials, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin generating idiotypic antibodies. The humanised antibody has a half-life in the human circulation essentially equivalent to that
                                                                                                                                                                                                                                                         This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody
                              of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                     Claim 25; Fig 6; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                   asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                Uses of humanised alpha-4 integrin antibody -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-1996;
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97..106
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    of human kappa light chain J region"
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/note- "21.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Leger OJ, Saldanha J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "REI Val-58 is substd. by Ile of mouse 21.6 VL, important in supporting the CDR2
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               (ATHE-) ATHENA NEUROSCIENCES INC
                                         21-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised alpha-4 integrin antibody 21.6 VL version La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIOMTOSPSSLSASVGDRVTITCKTSODINKYMAWYQOTPGKAPRLLIHVTSALOPGIPS 60
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                                         95US-0561521
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                                                                                                                                                                                                                                          /label- CDR2
/note- "21.6
77..108
                                                                                                                                                                                                                                                                                                                   /note-
                                                                                                                                                                  /note= "21.6 complementarity determining region
117..126
                                                                                                                                                                                                    109..116
                                                                                                                                                                                                              /note= "REI framework region
                                                                                                                                                                                                                              /label- FR3
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Pred. No. le-36;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also AAW22412). It is composed of complementarity determining regions from the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human REI framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used to produce a claimed humanised 21.6 Treating asthma aftercard production and the machinement for treating asthma aftercard productions.
           Region
                                                           Region
                                                                                                            Region
                                                                                                                                                                        Key
                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                      02-APR-1996
                                                                                                                                                            Region
                                                                                                                                                                                                                         antibody engineering
                                                                                                                                                                                                                                                        Mouse anti-VLA-4 antibody 21.6 light chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 equivalent to that of naturally occurring human antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Fig 10; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uses of humanised alpha-4 integrin antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                          81 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 126
                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones ST,
                                                                                                                                                                                                                                                                                   (first entry)
            50..56
                                                           35..49
                                                                                                                    /label- CDR2
                                  /note-
                                                 /label- FR2
                                                                                               /label- CDR1
                                                                                                                                               /label= FR1
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                     "mouse light
region 2"
                                                                     "mouse light chain variable
determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 562; DB 18;
Pred. No. 1.2e-36;
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                                  chain variable
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DB 18;

The humanised

Indels

0;

Gaps

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complementarity

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RESULT
AAR81326
ID AAR8
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                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                     The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain variable region (without signal sequence). Cloned cDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and the 2*CL antibody for the heavy chain in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are condified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, CC acid present in the equivalent position of the mouse 21.6 Ig light chain. Plasmids encoding the chimeric antibodies are transfected into CC cells. The humanized antibodies can be used to inhibit adhesion of as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
 AAR81326 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 66; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-1995;
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                                                                                                                                                                                                                                                                                                           anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory disease.
                                                                                            61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                   Local Similarity
                                                                            61
                                                                                                                                                                      1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                        1 digmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips
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                                                                           rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik
                                                                                                                                                                                                      94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones TS,
                                                                                                                                                                                                                                                                                106 AA;
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0186269
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    region 4"
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                                                                                                                                                                                                                 90.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FR4
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region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           determining
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   126 AA.
                                                                                                                                                                                                     6
                                                                                                                                                                                                                 Score 508; DB 16;
Pred. No. 1.5e-32;
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chain variable complementarity region 3"
                                                                                                                                                                                                      6,
                                                                                                                                                                                                                                   Length 106;
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cDNA sequences of mouse 21.6 VL and VH (see AAQ)9892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ)9895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L58 and L69 in the humanized light chain, anino acids L45, L61 amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and the treat inflammarry diseases such as multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse VLA-4 antibody 21.6 light chain variable region.
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                                                to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ99889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-1994;
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anti-idiotype antibodies.
                               detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents the mouse antibody 21.6 light chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ATHE-) ATHENA NEUROSCIENCES INC
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109..1
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21..43
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117..12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "signal peptide"
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61 RFSGSGSGRDYTFTISSLOPEDIATYYCLQYDNLWTFGQGTKVEIK 106

21 diqmtqspsslsaslggkvtltcktsqdinkymawyqhkpgkrprllihytsalqpgips 80

1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYOOTPGKAPRLLIHYTSALQPGIPS 60

Matches Best Query Match

94;

Conservative

6

5

Gaps

0

Local

Similarity

90.4%;

Score 508; DB 16; Pred. No. 1.8e-32; Mismatches

Length 126; Indels

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-1996 (first entry)
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The sequence represents the human reshaped antibody 21.6 light chain variable region against leukocyte adhesion molecule ViA-4. Cloned cDNA sequences of mouse 21.6 VL (AAO99889) and VH (AAO9892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAO99895-98) and
                                                                                                                                                                                                                            25-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                    Region
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                                                                                                                                                                                                     (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                             New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                  N-PSDB; AAQ99893
                                                                               Disclosure; Fig 10; 105pp; English.
                                                                                                     inflammatory disease
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70..76
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                                                                                                                                                                                                                                                                                                                                                                                      "complementarity determining region
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                                                                                                                                                                                     Saldanha J;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids 145, 149, L58 and L69 in the human kappa LC vR chain, amino acids 145, 149, L58 and L69 in the human kappa LC vR chain, amino acids the position of the mouse 21.6 Ig L chain. Plasmids encoding the position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an enotyphelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, menigitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity antibodies can also be used for detecting VLA-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purification or for generating anti-idlotype antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW22409 standard; Protein; 126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-4 integrin mouse MAb 21.6 VL region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               acute leukocyte mediated lung injury; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 diqmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips 80
                                               Region
                                                                                            Region
                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                      /label- Leader
21..43
                                                                                                                                                                                                                                           /note=
55..69
                                                  /note= "complementarity determining region
117..126
                                                                                                                                                                                                                                                                                                    /note= "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                       /label= CDR1
                                                                                                                                                                                                                                                                                                                       /label- FR1
                /note- "framework region 4"
                                                                                                             /note- "framework region
                                                                                                                                                                              /label- CDR2
                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                          /label- FR2
                                 /label= FR4
                                                                                                                              /label- FR3
                                                                                                                                                             note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.4%;
                                                                                                                                                                                                                                                        "complementarity determining region 1"
                                                                                                                                                              "complementarity determining region
                                                                                                                                                                                                            "framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 508; DB 16;
Pred. No. 1.8e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 126;
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AC XX XX AC XX XX AC XX XX AC XX XX AC XX XX AC XX XX AC XX XX AC XX XX AC XX XX AC 
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AAY29913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human MCP-3 and murine scFv38 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-1999 (first entry)
                                                                                      W09946392-A1
                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                      Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY29913 standard; Protein; 359 AA.
                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                incorporated into a human REI framework to produce a claimed humanised 21.6 VL (see AAW22412) and a claimed humanised incoment for dementing a disease selected from asthma, atherosclerosis, AIDS, arthritis, transplant rejection, graft versus host disease, tumour incomentatis, atopic dermatitis, psoriasis, myocardial metastasis, nephritis, atopic dermatitis, psoriasis, myocardial metastasis, nephritis, atopic dermatitis, psoriasis, myocardial may also be used in the affinity purification of alpha-4 integrin generating idiotypic antibodies. The humanised antibodies of the invention have a half-life in the human calculation essentially
                                                                                                                                                                                                                                                                                                                                  immune response; HIV; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This polypeptide comprises the light chain variable region (VL) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VL can be incorporated into a human REI framework to produce a claimed to the complementary of the com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 68; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma, atherosclerosis, AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uses of humanised alpha-4 integrin antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 rfsgsgsgrdysfnisnlepediatyyclgydnlwtfgggtkleik 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGGGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 digmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09718838-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0561521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US18807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.4%; Score 508; DB 18; 88.7%; Pred. No. 1.8e-32; tive 6; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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XX

PF 12-MAR-1999; 99WO-US05345.

XX

PR 12-MAR-1998; 98US-0077745.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Kwak LW, Biragyn A;

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Kwak LW, Biragyn A;

XX

PY New fusion polypeptides comprising a chemokine and a tumour antigen or preventing HIV antigen, used for treating cancers or treating or preventing HIV XX

PT HIV antigen, used for treating cancers or treating or preventing HIV XX

PT New fusion polypeptides comprising a chemokine comprise; (1) human monocyte chemotactic protein-3 (MCP-3) and human fusion proteins and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise; (1) human monocyte chemotactic protein-3 (MCP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human proteins and HIV gpl20; (6) human Muc-1; (5) human monocyte chemotaine (WDC) and human Muc-1; (5) human monocyte chemotaine (WDC) and human Muc-1; (C) SDF-1 and human MUc-1; (5) human IP-10 and HIV gpl20; (6) human MCP-3 and CC gpl20. The fusion proteins and nucleotide sequences encoding them, can response, free vision proteins, and nucleotide sequences encoding them, can cresponse. They can also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences for identifying unknown tumour antigen epitopes and fine mapping of cumour antigen epitopes. The present invention.

So Sequence 359 AA;
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Qγ
                                                                                        DЬ
 RESULT
                                      B
                                                                                                                                        Matches
                                                                                                                                                                 Query Match
                          233 digmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 292
                                                   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                   госат
                                                                                           1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
9
                                                                                                                                        90;
                                                                                                                                                  Similarity
                                                                                                                                     Conservative
                                                                                                                                            86.8%; Score 488; DB 20; 84.9%; Pred. No. 1.7e-30;
                                                                                                                                 9; Mismatches
                                                                                                                                                         Length 359;
                                                                                                                              Indels
                                                                                                                              0;
                                                                                                                            Gaps
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12-MAR-1998;
                     12-MAR-1999;
                                        16-SEP-1999.
                                                           WO9946392-A1
                                                                                                                     Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
                                                                               Synthetic.
                                                                                               Homo sapiens
                                                                                                                                         Human IP-10 and murine scFv38 fusion protein.
                                                                                                                                                                   17-NOV-1999
                                                                                                                                                                                       AAY29911;
                                                                                                                                                                                                     AAY29911 standard; Protein; 361 AA.
                                                                                                                 immune response; HIV; infection
                                                                                                                                                                 (first entry)
98US-0077745
                   99WO-US05345
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RESULT 10
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Best Local
WPI; 1999-551418/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
                                                          Kwak Lw,
                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                    12-MAR-1998;
                                                                                                                                                                                                                         12-MAR-1999;
                                                                                                                                                                                                                                                                                 16-SEP-1999.
                                                                                                                                                                                                                                                                                                                                      W09946392-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Artificial synthetic construct protein SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein 3 (MCP-3) and human Muc-1; (2) human interferon induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV gp120. The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune response. They can also be used for treating cancer or treating or can be used in in vitro diagnostic assays, as well as in screening assays tumour antigen epitopes. The present sequence represents a fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             immune response; HIV; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY29916 standard; Protein; 374 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-551418/46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                 Biragyn A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                 98US-0077745.
                                                                                                                                                                                                                   99WO-US05345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 488; DB 20; Length 361;
Pred. No. 1.7e-30;
9; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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В

В

Method of treating solid or cystic tumours with antibodies - by administering monoclonal antibody Mel-14, having Fc deleted,

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AAR60627
ID AAR6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                             Bigner DD, Carrel S,
                                                                                 N-PSDB; AAQ73537
                                                                                                         WPI; 1994-316669/39
                                                                                                                                                                                                                      (ZALU/) ZALUTSKY M R.
                                                                                                                                                                                                                                                                             (BIGN/) BIGNER D D.
                                                                                                                                                                                                                                                                                                                                         19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09421294-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ME1-14 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR60627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV 9p120. The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune response. They can also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in sequences can be identifying unknown tumour antigen epitopes and fine mapping of tumour antigen epitopes. AAV2916 and AAZ21156 to AAZ21168 are sequences given in the SEQ ID LISTING in the present invention but which are not mentioned further within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MCC) and human Muc-1; (4) human MDC-1; (5) human FP-10 and HIV gpl20; (6) human MCP-3 and HIV gpl20; (7) human MDC and HIV gpl20; and (8) human SDF-1 and MCP-3 and HIV gpl20; (7) human MDC and HIV gpl20; and (8) human SDF-1 and MCP-3 and HIV gpl20; (8) human MDC and HIV gpl20; (8) human SDF-1 and MCP-3 and HIV gpl20; (8) human MDC and HIV gpl20; (9) human SDF-1 and MCP-3 and HIV gpl20; (10) human MDC and HIV gpl20; and (10) human SDF-1 and MCP-3 and HIV gpl20; (10) human MDC and HIV gpl20; and (10) human MCP-3 human MDC and HIV gpl20; and (10) human MDC and HIV gpl20; and HIV gpl20; and (10) human MDC and HIV gpl20; and (10)
                                                                                                                                                                                                                                                     (CARR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR60627 standard; Protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 117-118; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 diqmtqspssisaslggkvtitckasqdinkylawyqhkpgkgprll1hytstlqpg1ps 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                      93US-0033864
                                                                                                                                                                                                                                                                                                                                                                                             94WO-US02724.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 488; DB 20; Length 374; Pred. No. 1.7e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of the ME1-14 light chain. The protein monoclonal antibody which can be administered to treat solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           See also AAR60626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cystic tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        using injection or deposition in the cyst cavity
                                                                                                                                                                                                                                                                                                                                                                                                                                  050
                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                      complementarity determining region.
                                                                                                                                                                                                                                                                                                                                              variable region; antibody; OKT4A; heavy chain; CD4;
                                                                                                                                                                                                                                                                                                                                                                CD4-specific CDR-grafted light chain
                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                      AAR13050;
                                                                                                                                                                                                                                                                                                                                                                                                                      AAR13050 standard; Protein;
                                                                                                              W09109966-A
                                                                                                                                        Region
                                                                                                                                                           Region
                                                                                                                                                                            Region
                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                  Region
Jolliffe LK,
                                    21-DEC-1990;
21-DEC-1990;
                                                                         21-DEC-1990;
                                                                                          11-JUL-1991
                                                                                                                                                                                               Region
                                                       21-DEC-1989;
                 (ORTH ) ORTHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RESGSGSGRDYTETISSLQPEDIATYYCLQYDNLWTEGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      digmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllmhytstlqpgips 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rfsgsgsgrdysfsisnlepediatyyclgydnlltfgggtkleik 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
 Zivin RA,
                   PHARM CORP
                                    89GB-0028874.
90WO-GB02017.
90WO-GB02018.
                                                                          90WO-GB02015
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                               111..116
                                                                                                                                                                                                                                            /label- CDR 1
                                                                                                                                                                                                                                                                                 /label= signal sequence
                                                                                                                                                                    /label= CDR 3
                                                                                                                                                                                                        /label= CDR 2
                                                                                                                                                                                                                           /label= framework
                                                                                                                                                                                                                                                              /label- framework region
                                                                                                                               /label- kappa constant domain
                                                                                                                                                  /label= framework region 4
                                                                                                                                                                                       /label= framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.6%;
 Pulito VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 481; DB 15;
Pred. No. 2.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                         234 AA
                                                                                                                                                                                                                            region
  Adair JR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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   CCCCXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is an example of a CDR-grafted light chain of the invention. The constant regions are based on sequences of the human kappa constant domain, the signal sequence is derived from murine MAD 1872.3 and the CDR sequences are based on the murine OKT4A light chain CDRs. The recombinant antibody encoded by this sequence has affinity for CD4 similar to that of CKT4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New CD4 specific recombinant - complementarity determining region grafted antibody for treating graft rejection and T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1991-222914/30.
N-PSDB; AAQ12633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 8; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                            Light chain variable region for monoclonal antibody 23F8.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAR78970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR78970 standard; Protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See also AAQ12627-Q12632.
                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody; heavy metal; mercury; variable region;
                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-1995
                                                                                      New polypeptide(s) which bind heavy metals, esp. mercury - derived from monoclonal antibodies, used for detecting, removing, adding or
                                                                                                                                                                                                                                          27-JAN-1995;
Hybridoma antibodies have been produced with the spleen cells of BALB/c mouse that had received multiple injections of mercuric ions reacted with glutathione to produce a mercuric ion coordinate
                                                                          neutralising heavy metals
                                                                                                                          N-PSDB; AAQ97508
                                                                                                                                          WPI; 1995-275415/36.
                                                                                                                                                                                        (BION-) BIONEBRASKA INC
                                                                                                                                                                                                                   27-JAN-1994;
                                                                                                                                                                                                                                                                  03-AUG-1995
                                                                                                                                                                                                                                                                                          WO9520607-A.
                                                                                                                                                                                                                                                                                                                                        light chain.
                                                 Claim 23; Page 67-68;
                                                                                                                                                                 Lopez 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 rfsgsgsgteytftisslqpediatyycqqydnllftfgqgtklqi 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RESGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                 Wagner FW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                   94US-0187407
                                                                                                                                                                                                                                            95WO-US01199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.6%;
                                                     106pp; English.
                                                                                                                                                                   Wylie DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 475.5; DB 
Pred. No. 1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>,</del> 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC covalent compound which was covalently bound to keyhole limpet CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5, CC 5B6 and 3EB) were producing MAbs that were strongly positive against glutatione-mercuric ions but negative against glutathione CC without mercuric ions. RNA was isolated from hybridoma cells with CC by Mulv reverse transcriptase. The primers used for cDNA synthesis CC chain expressed by the hybridoma of interest, or to the 5' and of the CC they chappe domain. Some of the primers used for cDNA synthesis are CC they chappe domain. Some of the primers used for cDNA synthesis are CC transcriptase. The primer used for cDNA synthesis are CC crainle region of a particular antibody polypeptide was also used for PCR amplification of that variable region, in conjunction with CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences CC in AA097498-097510 and the deduced AA sequences in AAR79241-R79250 & CC and in the claims are different from the descriptions in the CC sequence listings. The descriptions in the sequence listings. The descriptions in the sequence listings are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                Reg 1 on
                                                                                              Region
                                                                                                                                               Region
                                                                                                                                                                                             Region
                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                        Antibody; light chain; kappa; variable region; K20; integrin; CD29; beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                         T cell activation; complementarity determining region; CDR
                                                                                                                                                                                                                                                                                                                                                                                                                          Murine monoclonal antibody K20 kappa chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR93159 standard; Protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 rfsgsgsgrdysfsisnpepediatyyclgydnslftfgsgtkleik 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGRDYTFTISSLOPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l diqmtqspsslsaslgykvtltckasqdinkylawyqhkpgkgprlllhytstlqpgips 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALOPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
/note= "complementarity determining region"
                             'label- CDR3
                                                                             /label≖ FR3
                                                       'note= "framework region"
                                                                                                note "complementarity determining region"
                                                                                                                            /label- CDR2
                                                                                                                                                    note "framework region"
                                                                                                                                                                                               /note= "complementarity determining region"
                                                                                                                                                                                                                                                   /note= "framework region"
                                                                                                                                                                                                                                                                    /label- FR1
                                                                                                                                                                          'label≖ FR2
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                         'label- CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 471.5; DB
Pred. No. le-29;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _DB 16; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
            24-JAN-1990;
                                        01-AUG-1990.
                                                                     EP380068-A.
                                                                                                                 Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
                                                                                                                                                  Variable region of murine AHT 107 light chain.
                                                                                                                                                                                 10-DEC-1990 (first entry)
                                                                                                                                                                                                                                       AAR06252 standard; protein; 128 AA
                                                                                                                                                                                                                    AAR06252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of the variable region of the kappa light chain from murine monoclonal antibody K20. The antibody recognises the beta 1 subunit (CD29) of integrins and inhibits activation and proliferation of peripheral T cells induced by anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target for humanisation; the humanised version may be useful as an immunosuppressant. In the humanisation process, the complementarity determining regions (CDRs) of a human antibody with framework regions 70-95% homologous to those of K20 were replaced by the K20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanisation of non-human immunoglobulin variable regions - for prodn. of humanised antibodies, esp. K20, e.g. as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 2A; 39pp; French.
                                                                                                                                                                                                                                                                                                        61 rfsgsgsgrdysfsisnlepediatyyclgyynlwtfgggtkleik 106
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       90EP-0101351.
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81.1%; Pred. No. 3.4e-29;
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Search completed: July 9, 2002, 15:40:36 Job time: 122 sec
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24-JAN-1989;
                                                                                                                                                                                                                                                    MAbs comprising mouse CH and CL constant regions whith human variable regions may be used to create mouse/human hybrid MAbs, which have a longer serum half-life. Method can be used to produce Abs against interleukin-2 receptor and tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                            Expression vectors for producing chimeric monoclonal antibodies which express human constant region and non-human variable region
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N-PSDB; AAQ05556.
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                                                                                                                                                                                                                                Sequence 128 AA;
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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124.897 Million cell updates/sec
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Copyright (c) 1993 - 2000 Comp
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PCT-US95-01219-7
US-08-561-521-5
PCT-US95-01219-5
PCT-US95-01219-15
US-08-561-521-15
PCT-US95-01219-15
US-08-818-366-22
US-08-88-366-22
US-08-235-838-16
US-08-235-838-16
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US-08-465-4738-11
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US-08-602-725-29
US-08-561-521-8
PCT-US95-01219-8
US-08-875-611-57
US-08-875-611-57
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PCT-US93-07832-17
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ainst Leukocyte and Crew Suite 2000	Sequence 71, Appl Sequence 71, Appl Sequence 6, Appl Sequence 15, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 9, Appl Sequence 2, Appl Sequence 3, Appl Sequence 1, Appl Sequence 1, Appl Sequence 47, Appl

Query Match

Best Local Similarity

100.0%;

Score 562; DB 2; Pred. No. 1.2e-45;

Length 106

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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/186
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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                                                                                                                                                                                                                              Local Similarity
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OPERATING SYSTEM:
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                         100.0%; Score 562; DB 5; 100.0%; Pred. No. 1.2e-45;
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RESULT 4
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; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                          CORRESPONDENCE ADDRESS:
                                                                         TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                          APPLICANT: APPLICANT:
                                                                NUMBER OF SEQUENCES:
                                                                                                                       APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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NAME: Smith, William L.
REGISTRATION NUMBER: 30,
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APPLICATION NUMBER:
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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          STREET:
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                        ADDRESSEE:
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Local Similarity 88.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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STRANDEDNESS: sir
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STATE: California
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    3: Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Tower, Suite 200
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                                                                                                                 Leger, Olivier J.
Saldanha, Jose
Jones, S. Tarran
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                                                                                                                                                                            Bendig, Mary M.
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25-JAN-1994
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Steuart Tower, Suite 2000
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US-08-561-521-2
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FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, william L.
REGISTRATION NUMBER: 30,22:
REFERENCE/DOCKET NUMBER: 1!
    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                  APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
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TELEPAX: 415-543-5043
INFORMATION FOR SEC. 5:
                                                                                                                          COMPUTER READABLE FORM:
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LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
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COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
FILING DATE:
                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                      STREET: One Market F
CITY: San Francisco
STATE: California
                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                    California
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linear
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                                                                                                        Floppy disk
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TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: SMILD, WILLIAM L.
REGISTRATION NUMBER: 30, 223
REFERENCE/DOCKET NUMBER: 15:
                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: SMITH, WILLIAM L.
REGISTRATION NUMBER: 30;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
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                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release *1 ^
                                                                                                                                                                                                                                       CLASSIFICATION: 424
                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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TOPOLOGY: linear; MOLECULE TYPE: protein US-08-561-521-15
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Best Local !
                                                                     Matches
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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TELEPHONE: 415-543-9600
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                                                                                                                                                                                                           TYPE:
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Local Similarity
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                                 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                         linear
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88.7%;
                                                                                     90.4%;
88.7%;
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                                                                     6; Mismatches
                                                                     Score 508; DB 5; Length 126; Pred. No. 1.5e-40; 6; Mismatches 6; Indels
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; GENERAL INFORMATION:
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                                                          US-08-339-582-4
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Sequence 4, Application US/08339582
Patent No. 5558852
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                 Query Match
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INFORMATION FOR SEQ ID NO: 15:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Humanized Antibodies AGITITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY_AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE COMPATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: PATENTIA RELEASE #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acid
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TELEPHONE: 415-543-9600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                  90.4%; Score 508; DB 5; Length 126; BB.7%; Pred. No. 1.5e-40;
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APPLICANT: APPLICANT: APPLICANT:

Bigner, Darell D. Zalutsky, Michael R. Carrel, Stefan

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PRIOR APPLICATION NUMBER: US 08/033
APPLICATION NUMBER: US 08/033
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 919-881-31/5
INFORMATION FOR SEQ ID NO: 4:
       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                         NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
                                                                                                                                                                                                                   APPLICANT: Wylle, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         APPLICANT:
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MEDIUM TYPE: Floppy
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/08235838 Patent No. 5571894
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          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,838
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies
TITLE OF INVENTION: Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Mari
APPLICANT: Groner, Bernd
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FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
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                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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TYPE: a
FILING DATE:
                                                                                                                                        ZIP:
                                                                                                                                                 COUNTRY:
                                                                                                                                                                  CITY: Hawthorne
STATE: New York
                                                                                                                                                                                          ADDRESSEE: CIBA-GAZO.
CHREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 612-332-9081
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nes 89; Conservative
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REFERENCE/DOCKET NUMBER: 86
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th, Ina-Maria
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                                                                                                                                                                                                                                                                                     Recombinant Antibodies Specific for a
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Pred. No. 3.1e-37;
9; Mismatches 8;
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CLASSIFICATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Recombinant Antibodies TITLE OF INVENTION: Growth Factor Receptor NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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FILING DATE: 05-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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REGISTRATION NUMBER: 36,
                                                                                                                                   CLASSIFICATION:
                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 07901-6940
                                                                                                                                                                                                                                                                                                                                                                         CITY: Summit
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                                                                                                                                                                          APPLICATION NUMBER:
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Zwickl, Markus
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                                                                                                                                                    5 June 1995
                                                                                                                                                                                                                                                                     Floppy disk
                  UMBER: GB 91-810079.3
05-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nancy E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.9%; Score 460; DB 1; 80.2%; Pred. No. 2.6e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. 5939531man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant Antibodies Specific for a
                                                                                                                                                                              US/08/465,473B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08235838 Patent No. 5571894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (908)522 6955 INFORMATION FOR SEQ ID NO:
                                                                  FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION UNMEER: 36,129
REFERENCE/DOCKET NUMBER: 4-18
TELECOMMUNICATION INFORMATION:
                 TELEFAX: (919)541-868 INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
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LENGTH: 637 amino acids
                                                                                                                                                                                                       FILING DATE: 31-JAN-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/828,832
APPLICATION NUMBER: US 07/828,832
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Recombinant Antibodies
TITLE OF INVENTION: Growth Factor Receptor
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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nes 85; Conserv
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                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/235,838
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                                                                                                                                                                                       APPLICATION NUMBER:
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                                     (919)541-8689
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                                                        (919)541-8614
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                                                                                                                                                                                         GB 91-810079.3
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US-08-465-473B-11
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                                                                                                                                                                                   FILING DATE: 05 FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfelffer, Hesna J.
REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4-18:
TELECOMMUNICATION INFORMATION:
TELECHONE: (908)522 6940
                                                                                                                                     TELEFAX: (908)522 6955
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
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                                                                TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICANT:
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APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
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APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies
TITLE OF INVENTION: Growth Factor Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
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81.0%; Score 455; DB 1; Length 241;
Local Similarity 80.0%; Pred. No. 2.6e-35;
es 84; Conservative 10; Mismatches 11; Indeis
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                                                                                                   241 amino acids amino acid
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Harwerth, Ina-Maria
Groner, Bernd
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       81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Antibodies Specific for a
                                                                                                                                                                                                                                                                                                         GB 91-810079.3
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                                                                                                                                                       11:
Score 455; DB 2;
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Length 241;
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MOLECULE TYPE: per
HYPOTHETICAL: NO
FRAGMENT TYPE: N-1
ORIGINAL SOURCE:
ORGANISM: Hukan
US-08-602-725-29
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      Query Match 80.9%;
Best Local Similarity 83.0%;
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                  TELEFAX: 703-816-41UU
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/08602725 Patent No. 5965710
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/GB
FILING DATE: 19-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 931
FILING DATE: 21-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: YOUNG, SUSAN APPLICANT: BATES, PAUL A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                         TELEPHONE: 703-01.
TELEPHONE: 703-816-4100
                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 02-FEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241
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STATE: VA
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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                                                                                             Hukan REI light chain
                                                                                                                                                                                linear
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DURBIN, HELGA
SNARY, DAVID
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                                                                                                                                N-terminal
                                                                                                                                                              peptide
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02-FEB-1996
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 8; Mismatches
              Score 454.5; DB 2
Pred. No. 1.2e-35;
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Db 80

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Search completed: July 9, 2002, 15:39:04 Job time: 30 sec

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Tue Jul 9 15:50:39 2002
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OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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473.5
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Copyright (c) 1993 - 2000 Comp
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$49220
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S31999
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                         heavy chain V-1
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31 32 33 34 34 35 36 37 44 44 44 44 44 44 44 44 44 44 44 44 44
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127 135 126 108 108 143 125 129 129 127 127 127 127 127 127 127
PH0953 PH0953 PH0957 PH0957 PH0957 PH0957 PH0958 SB1170 A33548 S34014 S36260 PH1561 S23623 S38950 S40295 S40295 S40295
61 61 61 61 61 61 61 61 61 61 61 61
heavy
yy chain v r yy chain v r

ALIGNMENTS

Ig gamma chain (WM65) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S29594

submitted to the EMBL Data Library, February 1991 A; Reference number: \$29593 A; Accession: \$29594

A; Molecule type: mRNA A; Residues: 1-178 <SEY>

A; Status: preliminary

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C; Keywords: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment) (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (C; Species: 07-Sep-1990 *sequence_revision 07-Sep-1990 *text_change 20-Jun-2000 (C; Date: 07-Sep-1990 *sequence_revision 07-Sep-1990 *text_change 20-Jun-2000 (C; Accession: S03471; S07453
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A.Molecule type: mRNA
A.Residues: 7-120 <RCC1>
A.Residues: 7-120 <RCC1>
A.Cross references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983
A.Residues: 7-120 <RCC1>
A.Residues: 7-120 <RC1>
A.Re
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hypervariable regions.....
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                                                                                                                                                                                                                                                                                                        A; Reference number: S03471; MUID:84057768
A; Accession: S03471
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75.6%; Pred. No. 1.2e-36;
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R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Watl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expu
                                                                                                                                                     Ig heavy chain V-1 region (WIL2) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-118 <GRI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Human anti-self
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region (clone alpha-MUCl-1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: S36256; MUID:93178448
A;Recession: S36255
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A; Residues: 1-43 < ROC2>
C: Superfamily: immunoglobulin V region; immunoglobulin homology
C: Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE---GYYGNYGVYAMDYWGQGT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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76.2%;
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Pred. No. 1.
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1.8e-35;
ches 13; Indels 11; Gaps
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Ig heavy chain V region (E8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S17586
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr
                             R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>
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A; Molecule type: mRNA
A; Residues: 1-142 <LAR>
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A; Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells A; Reference number: A32483; MUID:89273586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C:Accession: A32483
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A; Residues: 1-123 <KIP>
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A;Accession: D33548
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
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73.2%; Pred. No. 8.1e-35;
8: Mismatches 22; Indels
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Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C.Accession: PH0954
R.Martin, T.: Duffy, S.F.: Carson, D.A.: Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
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A; Rosidues: 1-122 <MIL>
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J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (clone IIc) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: S06823
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A; Residues: 1-117 < MYL>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                           61 DPKFOGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY-YGNYGVYAMDYWGOGTLV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DPKFQDKATITADTSSNTAYLQLSSLTSEDTAVYYCA--GYDYGNF-----DYWGQGTTL 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.2%; Score 459.5; DB 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-116 < MON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, September 1991
A;Description: Cloning and sequencing of the cDNA coding for the variable regions of A;Reference number: $24287
A;Accession: $24289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 gamma chain V region (JS34/32) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
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A:Residues: 1-132 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F:51-67/Region: complementarity-determining 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:31-35/Region: complementarity-determining
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                                                                                                                                                                                                                                                                                                               Query Match
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114 VSS 116
                                        121 VSS 123
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                                                                     61 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARWAGYY------FDYWGQGTTLT 113
                                                                                                  62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                 1 VQLQESGAELVKPGASVKLSCTASVFNIQDTYMHWVRQRPKQGLEWIGRIDPANGNTHFD 60
                                                                                                                                                                                         2 VOLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQADGQRLEWMGRIDPANGYTKYD 61
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                                                                                                                                                                                                                                                                               69.5%; Score 455; DB 2; Length 116; 71.5%; Pred. No. 7.7e-34;
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72.0%;
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Pred. No. 6.5e-34;
1; Mismatches 27
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RESULT S49220

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submitted to the EMBL Data Library, September 1994
A; Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing
A; Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing
A; Reference number: S49220
A; Accession: S49220
A; Molecule type: mRNA
A; Residues: 1-221 <KIP>
A; Cross-references: EMBL: C37502; NID: g541778; PIDN: CAA85732.1; PID: g541779
A; Experimental source: strain Balb/c
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
C
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c;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 *sequence_revision 01-Aug-1997 *text_change 21-Jan-2000
C;Accession: $49220
C;Accession: $49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46393
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A; Residues: 1-129 <FIG>
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                                                                                                                                                                                                                                                 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREG--YYGNYGVYA----MDYWG 114
                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                    QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60
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                                                                                                                                                                  AQKFQGWVTMTRDTSISTAYMELSRLRSDDTAVYYCARDSAYYYDSSGYYSANYYMDVWG 120
    KGTTVTVSS 129
                                                                                   QGTLVTVSS 123
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70.7%;
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Pred. No. 1.5e-33;
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C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03482; S07453
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A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
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A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Cross-references: EMBL:X03219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: S03471; MUID:84057768
A;Accession: S03482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   503482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S07453; MUID: 83058021
A; Accession: S07453
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A; Molecule type: mRNA
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                                                                                                                                                                     A;Cross-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840 C;Superfamily: immunoglobulin V region; immunoglobulin homology F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                        R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D. submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-135 <MAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                                           A; Accession: S49530
                                                                                                                                                                                                                                                                                                                                                A; Reference number: S48797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DPKFQGKATITTDTSSNTAYLQFSSLTSEDTAVYYCARGTTVGR------DYWGQGTTLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVOLOOSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPAKGNTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                       Conservative
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70.2%;
                                                                              68.3%;
72.8%;
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                                                         7; Mismatches
                                                                              Score 447.5; DB 2;
Pred. No. 4.2e-33;
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                                                               16;
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                                                            Indels 11; Gaps
                                                                                                           Length 135;
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A:Reference number: PH0952; MUID:92202880
A:Accession: PH0960
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-136 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                          R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies
                                                                                                                                                                                                                                         19 heavy chain V region (G6+ T-L30) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: pH0960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A: Molecule type: mRNA
A: Residues: 10-120 <ROC1>
A: Cross-references: EMBL: X07144
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A:Accession: S07453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Status: preliminary
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A;Accession: S03484
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S03484
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                                                                                                                                                                                                                                                                                                                                                                                                                                        117 VSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GPKFQGXATITADTSSSAAYLQLSSLTŠGDTAVYYCTR----GWFRRDAMDYWGQGTSVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVOLOOSGAELVKPGÁSVKLSCTASGFNIKDTYMHWVKORPEQGLEWIGRIDPANXNSKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.2%; Score 447; DB 2; Length 120; 71.5%; Pred. No. 4.2e-33; ative 11; Mismatches 20; Indels
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Job time: 64 sec

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Search completed: July 9, 2002, 15:39:38
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F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
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F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;99-124/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: heterotetramer; immunoglobulin
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                                                                                        121 YGMDVWGQGTTVTVSS 136
                                                                                                                                108 YAMDYWGQGTLVTVSS 123
                                                                                                                                                              61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGRTRVSVSTLYDSSGYYDFSGY 120
                                                                                                                                                                                                        61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR------EGYYGNYGV 107
                                                                                                                                                                                                                                                                                                                                                      Local Similarity les 94; Conserv
                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
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69.1%; Pred. No. 5.3e-33;
ative 1; Mismatches 28
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Database :
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Perfect score:
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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        BLOSUM62
Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen
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        HV1H_HUMAN
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HV00_MOUSE
HV06_MOUSE
HV10_MOUSE
HV10_MOUSE
HV16_HUMAN
HV14_MOUSE
                  HV49_MOUSE
HV52_MOUSE
HV24_MOUSE
HV37_MOUSE
HV1D_HUMAN
HV38_MOUSE
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HV12_MOUSE
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HV1A_HUMAN
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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR----EGYYGNYGVYAMDYWGQ 115

QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY 79 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY

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	Ouery Match 65.3%; Score 427.5; DB 1; Lengti Best Local Similarity 64.1%; Pred. No. 6.3e-36; Matches 82; Conservative 16; Mismatches 25; Indel:	ELHUND. ; IMCP. ; IMCP. R003006; Ig_MHC. R003596; Ig_v. 7; ig; 1. 06; IGv; 1. 1 19 20 147 IG HEAVY CHAIN V-I REGION 20 20 PYRROLIDONE CARBOXYLIC ACI 21 21 T -> V (IN REF. 2). 23 54 IH -> HI (IN REF. 2). 26 68 VG -> GV (IN REF. 2). 27 147 28 MISSING (IN REF. 2). 18 147 147 147 147 147 147 147 148 159 16491 MW; 948F9F72A5366C20 CRC64;	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-83065234; PubMed-6815656; Kenten J.H., Molgaard H.V., Houghton M., Derbys Bell L.O., Gould H.J.; "Cloning and sequence determination of the gene immunoglobulin epsilon chain expressed in a mye Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982 [2] SEQUENCE OF 20-147. Bennich H.H., Johansson S.G.O., von Bahr-Lindst. [In] Bach M.K. (eds.); Inmediate hypersensitivity: modern concepts and Marcel Dekker, New York (1978). -i- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLA' PROTEIN.	SULT 1 IC_HUMAN HVIC_HUMAN FO1744; 21-JUL-1986 (Rel. 01, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) 17 heavy chain V-I region ND precursor (Fragments). 18 homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBL_TaxID-9606;	38 315 48.1 123 1 HV21B_MOUSE 39 314.5 48.0 122 1 HV21B_MOUSE 40 314 47.9 117 1 HV05_MOUSE 41 313 47.8 123 1 HV25_MOUSE 42 313 47.8 123 1 HV01BAT 43 312 47.6 118 1 HV01BAT 44 312 47.6 123 1 HV31B_HOUSE 45 311.5 47.6 122 1 HV31B_HUMAN 47 312 47.6 122 1 HV31B_HUMAN 48 311.5 47.6 122 1 HV31B_HUMAN
1790 1794 1809 1809 1791 1769 110 Vin Vin WYE. 5;	DB 1; 3e-36; s 25;	IN V-I REGION CARBOXVLIC AC CEF. 2). REF. 2). REF. 2). REF. 2). REF. 2).	rbyshire R.B., gene for the h myeloma cell 1982) ndstrom H., and developme	7 AA. ate) pdate) (Fragments). Vertebrata; Euteleostomi 1; Hominidae; Homo.	P01787 P01790 P01749 P01805 P01805 P01809 P01791 P01769

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Best Local :
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region 36-65.
                                                                                                                                                                 _MOUSE
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma NON_TER 120 120
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                                                      HV07_MOUSE STANDARD; PRT; 139 AA.

P01751; P01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38 B1-8/186-2 precursor.

Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1023-1032(1982).

-i- mISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Siekevitz M., Gefter M.L., Brodeur P., Marshak-Rothstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV03_MOUSE
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                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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              NCBI_TaxID=10090;
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A02028; HVMSG7.
P01789; IMCP.
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120 AA;
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                                            Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                             62.4%;
63.1%;
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DOMAIN
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pfam; PF00047; ig; 1.
smarT; sm00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibodies: somatic mutation evident in a
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                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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MEDLINE-83144028; PubMed=6298778;
                          SEQUENCE FROM N.A.
                                                                        NCBI_TaxID=9606;
                                                                                                Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                        HV1B_HUMAN
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                                                                                                                                                                             heavy chain V-I region HG3 precursor.
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JH2 SEGMENT.
BY SIMILARITY.
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Pred. No. 4.7e-34;
8; Mismatches 25
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COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                Craniata; Vertebrata; Euteleostomi;
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                                                                                                          Hominidae;
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                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
InterPro; IPR003006; Ig_MHC
InterPro; IPR003596; Ig_v.
                                                          PIR; A02028; HVMSG7.
                                                                                                                                                or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capra J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-82152818; PubMed~6801765; Sims J., Rabbitts T.H., Estess P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                           InterPro;
                                                                                   EMBL; J00493; AAA38128.1; -.
                                                                                                                                                                  entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                   Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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Byolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003006;
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Pred. No.
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Score 396; DB 1; Pred. No. 6.8e-33;

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SEQUENCE
                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HV1G_HUMAN STANDARD; PRT: 117
P23083;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence upda
15-JUL-1999 (Rel. 38, Last annotation up
19 heavy chain V-I region V35 precursor.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
SIGNAL 1 19
CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
NON_TER 140 140
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                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          EMBL; X07448; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 7:1047-1051(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                      13009 MW; BE61CE63F8CE97BD CRC64;
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Pred. No. 4.2e-33;
                                                                                                                  IG HEAVY CHAIN V-I REGION V35
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SEQUENCE
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21-JUL 1986 (Rel. 01, Last sequence update)
15-JUL 1999 (Rel. 38, Last annotation update)
1g heavy chain V-I region EU.
Homo sapiens (Human).
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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Cunningham B.A., Rutishauser U., Waxdai M.J., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 9:3188-3196(1970).
-!- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1
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InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                          61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-----GGYGIYSPEEY-NGGLVT 114
                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY
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                                                                                                                                                                                                                                                                                            OVQLVQSGAEVKKPGSSVKVSCKASGGTESRSAIIWVRQAPGQGLEWMGGIVPMFGPPNY
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117
117 AA;
(Rel. 01, Created)
(Rel. 01, Last sequence up
(Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                       STANDARD;
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117
12472 MW;
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Pred. No. 2.7e
8; Mismatches
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Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HV51_MOUSE
                                                                                          SMART;
                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                               NCBI_TaxID-10090;
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Immunoglobulin V region.
DOMAIN 98
DOMAIN 99 104
DOMAIN 105 118
DISULFID 22 96
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Nature 283:35-40(1980).
-i- MISCELLANEOUS: THE SEQUENCES OF 10 HYPDTROWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIJINE-84182519; PubMed-6201362; Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.; Paidrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.; Paidrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.; Paidrop R., Bovens J., Rajewsky K.; Paidrop Revenue Rajewsky K.; Paidrop Revenue Rajewsky R., Rajewsky K.; Paidrop Revenue Rajewsky R., Rajewsky K.; Paidrop Revenue Rajewsky R., Rajewsky K.; Paidrop Revenue Rajewsky R.; Paidrop Rajewsky R.; Paidrop Revenue Rajewsky R.; Paidrop Rajewsky R.; Paidr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region AC38 205.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 WHICH OCCUR IN THE D AND J SEGMENTS.
-I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                        InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                        A02040; MHMS38.
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                                                                                                                                                                                                                      PF00047; ig; 1.; sm00406; igv; 1.
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117
117 AA;
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    V SEGMENT.
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J SEGMENT.
BY SIMILARITY.
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Pred. No. 4.3e-31;
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Best Local :
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region MOPC 104E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete amino acid sequence of a mouse mu chain: homology heavy chain constant region domains.";
Biochemistry 21:5415-5424(1982).
-1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS I PROTEIN HAS ALSO BEEN DETERMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83075344; PubMed-6816276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HV12_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - I - MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 VSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Loca L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NQKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCAR-----GYGYDPFDVWGTGTTVT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                           121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGKSLEWIGDINPNNGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMCRIDPANGYTKY 60
                                                                                                                   61
                                                                                                                                                                           61
                                                                                                                                                                                                                                   1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60
                                                                                                                                                                                                                                                                  1 OVOLVOSGAEVKKPGASVKVSCKASGENIKDTYIHWVROAPGORLEWMGRIDPANGYTKY 60
                                                                                                                   NOKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARD----YDWY-FDVWGAGTTVT
                                                                                                                                                                        DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA; 12983 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12934 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.3%;
58.5%;
                                                                                                                                                                                                                                                                                                                                                                                     56.9%; Score 373; DB 1; Length 117; 59.3%; Pred. No. 1.4e-30;
                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 375.5; DB 1
Pred. No. 7.7e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3CF8ACE4BE447E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 118;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THIS IGM MYELOMA
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RESULT 11
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RESULT 12
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Best Local
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P01755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-81234548; PubMed-6788376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region S43 precursor
                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003596; Ig_v. pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J00539; AAA38172.1; -. PIR; A02038; G2MS43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibodies: somatic mutation evident in a gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Heavy chain variable region contribution to the NPb family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baltimore D.;
                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                             DOMA I N
                                           135
                                                                      121 VSS 123
                                                                                                                                                                                                                Local Similarity
hes 74; Conserv
                                                                                                 80
                                                                                                                            61
                                                                                                                                                        20
                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGORLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 24:625-637(1981).
MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NPB ANTIBODIES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                               NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARY-RLGRY----FDYWGQGTTLT 134
                                                                                                                          DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                       QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY
                                           VSS 137
                                                                                                                                                                                                                                                                                     137
137 AA;
                                                                                                                                                                                                                 Conservative
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54
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122
137
                                                                                                                                                                                                                                                                                     15200 MW; ADD5881BF44B8EC9 CRC64;
                                                                                                                                                                                                                            56.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig_MHC.
                                                                                                                                                                                                                 14; Mismatches
                                                                                                                                                                                                                               Score 371.5; DB 1
Pred. No. 2.3e-30;
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COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                              D SEGMENT
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                                                                                                                                                                                                                                                                                                                                JH2 SEGMENT
                                                                                                                                                                                                                                                                                                                                                           FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK - 2
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                                                                                                                                                                                                                                                                                                                   SIMILARITY
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                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                    30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2a variable
                                                                                                                                                                                                                                            Length 137;
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HV48_MOUSE

HV48_MOUSE

STANDARD;

138 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                         101-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 heavy chain V region AC38 15.3.
                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
'A V region determinant (idiotope) expressed at high frequenc lymphocytes is encoded by a large set of antibody structural EMBO J. 3:517-523(1984).
                                MEDLINE=84182519; PubMed=6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
Dildrop R., arterminant (idiotope) expressed at high frequency i
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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NON_TER
SEQUENCE
                                                                                                                         SEQUENCE
                                                                                                                                                                 NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                 HV50_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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23 - CCT-1986 (Rel. 02, Created)
23 - CCT-1986 (Rel. 02, Last sequence update)
15 - JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region TEPC 1017 precursor.
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SMART; SM00406; IG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. S
PIR; A02033; HVMST7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Illegitimate recombination generates a class switch delta in an IgD-secreting plasmacytoma."; Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 TVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tucker P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gilliam A.C., Shen A., Richards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFSA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCARSDGYYDWF-----VYWGQGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVOLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRPGQGLEWIGEINPNDGRSNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138
138 AA;
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86
118
128
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                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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138
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58.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 369; DB 1;
Pred. No. 4.1e-30;
0; Mismatches 26
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COMPLEMENTARITY-DETERMINING-1
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Best Local
                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
NON_TER 121 121
                                                                                                                                                                                                                                                                       "Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
19 heavy chain V region MPC 11.
Mus musculus (Mouse)
                                                                                                                                                                                                                Nucleic Acids Res.
                                                                                                                                                                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                            PIR; A02027; GVMS1
                                                                                                                                                                                                                                         Zakut R., Cohen J.,
                                                                                                                                                                                                                                                     REVISIONS.
                                                                                                                                                                                                                                                                                                               Zakut R., Cohen J.,
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=81053741; PubMed=6253904;
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Pfam; PF00047; ig; 1.
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Immunoglobulin V region.
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                     1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY
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EAQLQQSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY
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                                                           Similarity
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69; Conserv
                                                                                                            121 AA;
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THIS SEQUENCE WAS TR
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105
120
96
120
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55.3%;
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56.1%;
                                                23; Mismatches
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                                                          Score 360; DB 1;
Pred. No. 2.8e-29;
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Pred. No. 9.8e-30;
9; Mismatches 32
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Sciurognathi; Muridae; Murinae; Mus
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PIR; A02042; HVMSB1
HSSP; P01772; 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1
SMART; SM00406; IGv; 1.
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NON_TER 136 136 IG HEAVY CHAIN V REGION B
SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/orsend an email to license@isb-sib.ch).
134 VSS 136
                                                        121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by two adjacent CH genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Simultaneous expression of immunoglobulin mu and delta heavy chains
by a cloned B-cell lymphoma: a single copy of the VH gene is shared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                80 NOKEKGKATWTVDKSSSTVHMELARLTSEDSANLYCAR--YYGNY----FDYWGOGTTLT 133
                                                                                                                                                     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                     20 QVQLQQSGPEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYNGNTSY 79
                                                                                                                                                                                                                                                                             1 OVOLVOSGAEVKKPGASVKVSCKASGENIKDTYIHWVROAPGORLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                 55.0%; score 360; DB 1; Length 136; 56.9%; Pred. No. 3.2e-29;
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Search completed: July 9, 2002, 15:45:57

Job time: 373 sec

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Result
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Copyright (c) 1993 - 2000 Compugen Ltd
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+03	100	494	144	143	146	463	143	157	117	118	141	139	143	137	488	145	143	481	500	150	142	145	143	140	145	117	143	142	473
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Q90 E70	001176	0001.26	0924P5	092405	092408	Q99LC4	Q91V67	095978	Q9QXF0	Q9Z1C4	Q924Q4	Q924R5	Q91VA2	Q924R6	Q91WR1	Q924R3	Q924R7	Q91WT1	Q9BRV0	094298	Q924Q2	Q924P7	Q924R0	Q924R2	Q924Q9	Q9QXE9	Q924P9	092401	Q99L25
Q9)175 mus musculu	Caarge was wascard	E C			2	80	Sum	OMO	Bull					1 2	A .		Bug	i s	ĕ		200			2	nus mus	25	mus.	_	Q99125 mus musculu

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SEQUENCE
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09UL92;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998). EMBL: AF035022; AAD56258.1; -. HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLLNE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fetus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young D.C.;
                                                   1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 60
                                                                                                                                                                                                                                                                                                                                                         124
124 AA;
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                  124
; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                69.8%;
69.5%;
                                                                                                                                                                9;
                                                                                                                                                                                        Score 457.5; DB 4; Length 124; Pred. No. 3.8e-41;
                                                                                                                                                         Mismatches
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RESULT OPPLIANT OF STANFORM OF
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Best Local S
Matches 87
              Submitted (FEB-2001) to the EMEMBL; BC003878; AAH03878.1; -. HSSP; P01842; 7FAB.
InterPro; IPR003599; Ig..
InterPro; IPR003597; Ig_1.
InterPro; IPR003600; Ig_1ike.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_WHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
pUTATIVE MATRIX CELL ADHESION MOLECULE-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q96QS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 099L31 PRELIMINARY; PRT; 468 AA.
099L31;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 WGQGTLVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR-----GLYVVVPAAFSRFDY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WGQGTLVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDYWGQGTLVTVSS 123
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PF00047; ig; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
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Best Local :
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Best Local Similarity
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SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
SMART; SM004010; IG_Like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20448942; PubMed-10992488;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
EMBL: AF206021; AFF69319.1; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9JL85;
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003006; Ig_MHC: InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01810; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 VSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 EVOLOQSGAELVRPGASVKLSCTASGFNIKDSLMHWVKQRPEQGLEWIGWIDPEDGETKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                    61
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                                                                                                                                                                                                                                 AELVKPGASVKLSCTASGFNIEDTYMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKA
                                                                                                                TITSDTSSNTAYLQLSSLTSEDTAVYYCVRR---
                                                                                                                                                                         TITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVTVSS 123
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109
109 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11944 MW; DFE615FE6CED4EDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.2%; Score 440; DB 11; 67.5%; Pred. No. 1.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                              66.0%;
68.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                  15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Score 432; DB 11;
Pred. No. 1.7e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                -GAVVFDYWGQGTALTVSS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 109;
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                                                                        Query Match
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Best Local
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                                                                                          Strausberg R.;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009851; AAH09851.1; ...
SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                             Q96GA6;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:15420).
Homo sapiens (Human).
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                      TISSUE-PRIMARY B-CELLS FROM TONSILS;
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                         NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                             Q96GA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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MEDLLNE=90277139; PubMed=9614934;

Wu X., Liu B., Van der Merwe P.L., Kalls N.N., Berney S.M.,

Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  117 VSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P01810; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AQKFQGKYTMTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLW----FDPWGQGTLVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         نسو
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       6
                                          88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVQLVESGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGOGLEWMGWINPNSWTTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunol Immunopathol 87:184-192(1998).
AF035020; AAD56256.1; -.
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R 1 1
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                                       Conservative
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                               66.0%; Score 432; DB 4; Length 614; 71.5%; Pred. No. 1.5e-37; vative 9; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.0%; Score 432; DB 4; Length 119; 70.7%; Pred. No. 1.9e-3B; tive 10; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                   614 AA.
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Q9UL95 PRELIMINARY; PRT; 125 AA.
Q9UL95;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00409; IG; 1
SMART; SM00406; IGV;
SMART; SM00410; IG_1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9GYZ2 PRELIMINARY; PRT; 119 AA.
O9GYZ2;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schistosoma japonicum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Song X.T., Feng Z.Q., Guan X.H.;
"Amplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 of
                                                                                                                                      117 VSS 119
                                                                                                                                                              121 VSS 123
                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; 19; 1
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InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P01772;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-6182;
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                                                                                                                                                                             61 NOKEKDRVTMTTDKSFSTAYMDLRSLRSADSAVYYCAR--YYDDH--YCLDYWGQGTTVT 116
                                                                                                                                                                                                   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                         Local
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82; Conserv
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119 AA;
                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                         119
13567 MW; BA893873FD5FA6AB CRC64;
                                                                                                                                                                                                                                                                                         65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig.
Ig_like.
                                                                                                                                                                                                                                                                            17; Mismatches
                                                                                                                                                                                                                                                                                    Score 428; DB 5; Length 119; Pred. No. 5e-38;
                                                                                                                                                                                                                                                                           20; Indels
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Best Local
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                                                                                                            Matches
                                                                                                                                      Query Match
Best Local
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF035019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recus
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01-DEC 2001 (TrEMBLrel. 19, Last sequence update)
01-DEC 2001 (TrEMBLrel. 19, Last annotation update)
VH186.2-D-J-C MU PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
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                                                                                                                                                                                                                                            NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                ROZONO Y., KOZONO H., AZUMA T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals

"Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Hydroxy-3-Nitrophenyl)Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q924Q3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                            EMBL; AB067797; BAB63282.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                  NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AQKVQGRVTMTRDTTISTAYMELSRLRSDDTAVYYCARSQGGGRIAAAGDAFDIWGQGTM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DPKFOGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY--AMDYWGQGTL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                      Local Similarity
                                                1, OVOLVOSGAEVKKPGASVKVSCKASGFNIKDTYIHWVROAPGORLEWMGRIDPANGYTKY 60
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QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu B., Van der Merwe P.L., Kalis N.N., Berney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunol. Immunopathol. 87:184-192(1998).
Immunol: AAD56255.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125
125 AA;
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                                                                                                                                                                                                                                                  146 AA;
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                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13516 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.3%;
68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig_MHC
                                                                                                                                                                                                                                                        16136 MW;
                                                                                                                                           65.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches
                                                                                                                    17;
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pred. No. 5.3e-38;
0; Mismatches 27;
                                                                                                                    Score 427; DB 11;
pred. No. 8.3e-38;
7; Mismatches 23;
                                                                                                                                                                                                                                                     CEA8DD6E1955807F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RA Arakawa I., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Jara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Jara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashizaki V.
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                                                                                                                                                  Query Match
                                                                                                                                    Best
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Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-DEC-2001 (TrEMBLrel. 19,
1810060009RIK PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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SMART; SM00409; IG; 2.

SMART; SM00407; IGC1; 3.

SMART; SM00406; IGV; 1.

SMART; SM00410; IGLike; 1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1

PROSITE; MO0410; AA; 51699 MW; 9DED:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001)
EMBL; AK007918; BAB25349
                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR003599; Ig.
Interpro; IPR003597; Ig_cl.
Interpro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:96443; Igh-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                    Local
61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                       1 QVOLVOSGAEVKKPGASVKVSCKASGENIKDTVIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                       P01842;
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                                                                                                                                    Similarity
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                                                                                                                                    64.4%; Score 422; DB 11; 65.9%; Pred. No. 1.2e-36;
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Last annotation update)
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                                                                                                                      19;
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                                                                                                                        Mismatches
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                                                                                                                                                              DB 11;
                                                                                                                          19;
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RESULT 12
Q924R1
ID Q924R1
AC Q924R1
DT 01-DEC
RT NCBILT
RN [1]
RR SEQUEN
RC STRAIN
RA KOZONO
RT "D1-ECC
RT Affini
RT Affini
DR EMBL;
FT NON_TE:
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Best Local
KOZONO Y., KOZONO H., AZUMA T.;

**Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP). *;

**Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.**
                                                                                                                                                                                                   Q924R1
Q924R1;
Q924R1;
Q924R1;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VH186.2-D-J-C MU PROTEIN (FRAGMENT).
                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                          STRAIN-C57BL/6;
                                                                                                                                                       NCBI_TaxID-10090;
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
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**Polifical Estimation of Relative Affinity by Flow Cytometry keveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP). *;

**Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.**

EMBL: AB067785; BAB63270.1;
                                                                                                                                                                                                                                                                                                                                                                                 118
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01-DEC-2001 (TrEMBLrol. 19, Last sequence update)
01-DEC-2001 (TrEMBLrol. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                             121 VSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q924R4
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Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus
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145 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 415.5; DB 11; Length 145;
Pred. No. 1.4e-36;
17; Mismatches 23; Indels 3;
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                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(FRAGMENT).
      MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
                                                                          Q9UL89;
                                                                                        687n60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0924R8 PRELIMINARY; PRT; 146 AA. 0924R8; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 01-DEC-2001 (TrEMBLEL. 19, Last annotation update) VH186.2-D-J-C MU PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl) Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                               119 VSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB067781; BAB63266.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteieosi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                            121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                               61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR-SYYGS-SLYYFDYWGQGTTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                           61 DPKFQGRVTTTADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
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                                                                                                                                                                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR---YDGSSFYAMDYWGQGTSVT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                     PRELIMINARY;
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15979 MW;
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                                                                                                                                                                                                                                                                                                                                       19;
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                                                                                                                                                                                                                                                                                                                                                Score 412; DB 11;
Pred. No. 3.3e-36;
                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                        92460F1FDF1B7538 CRC64;
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                                                                                   116 AA.
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Best Local 9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
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EMBL; AF035025; AAD56261.1; -.
HSSP; P01810; 2FBL;
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q924Q6 PRELIMINARY; PRT; 145 AA. Q924Q6; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) VH186.2-D-J-C MU PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; АВ067794; ВАВ63279.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 QGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY-AMDYWGQGTLVTVSS 123
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61. DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE--GYYGNYGVYAMDYWGQGTL 118
                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                    1 Similarity 63.2
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116 AA; 12605 MW; C8F9131DE13EA898 CRC64;
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Qy 119 VTVSS 123
Db 116 VTVSS 120
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Search completed: July 9, 2002, 15:45:36 Job time: 387 sec

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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Perfect score:
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Mouse anti-VLA 4
Mouse VLA-4 antibo
Alpha-4 integrin m
Heavy chain variab
A fusion of single
Human/murine chime
Chimaeric human/mu
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Humanised alpha-4
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nst VLA-4 - used for in lial cells, partic. for lish.	OJ, Saldanha J;	INC.						adhesion molecule; VI	heavy chain variable			123 AA.	ALIGNMENTS		AAY56877	AAR33953	AAR59942	AAB/4976 AAW21847	AAB74973	AAY52715	AAR47491 AAV52712	AAB74981	AAY52720	AAB74969	AAY52708	AAR92079	AAB74979 AAR57476	AAY52718	AAR92084	AAY52/19 AAB74980	AAB74978	AAK5/611 AAY52717	AAB07969	AAR81324 AAW22425	AAW22426	AAR81325	AAR76682 AAW04397	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
or treating								VLA-4; therapeutic;	region, Ha.					A01.10016	CDR-grafted humani	variable	Anti-VIAA rab burn	Humanised ATR-5 H	Humanised ATR-5 H	Humanised ATR-5 H	Humanised anti-CD1	Humanised ATR-5 H	Human Ab heavy cha	Humanised ATR-5 H	Humanized 1308F VH	CDR-grafted anti-R Murine 1308F VH Ch	Humanised ATR-5 H	Human 2*CL antibod Humanised ATR-5 H	Humanised ATR-5 H	Humanised ATR-5 H	Humanised ATR-5 H	hIL2R Ab H chain v	A heavy chain vari	VLA-4		himaeric human/m	-SNO	

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence encodes the mouse antibody 21.6 heavy chain variable region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions cDNA sequences of mouse 21.6 vL and VH (AAQ99889 and AAQ99895-99) and the mouse cDNAs are antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-99) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 mammalian cell expression vectors containing human kappa or gamma-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detecting VLA-4, for affinity purification or for generating
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                                                                                                                                                                                                                                                                                                                                                                   Human VLA-4 reshaped antibody 21.6 light heavy variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR81333 standard; Protein; 142 AA.
                                                                                                                                                                                                                                                                                                                         antibody engineering
                                                                                                                                                                                                                                                                                                                                    Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-1996
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                                                                                                                                                                                                                                                                                          Homo sapiens.
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50..54
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20..49
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                                /note= "complementarity determining region 3" 132...142
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                                                                                             .117
                                                                                                                                         "framework region 2"
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Pred. No. 5.5e-53;
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CC chain variable region against leukocyte adhesion molecule VLA-4.

CC cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ9889)

CC regions are linked to human constant regions in the construction

CC regions are modified using PCR primers (AAQ99892-98) and then

CC mouse cDNAs are modified using PCR primers (AAQ99895-98) and then

CC subcloned into mammalian cell expression vectors containing human

CC kappa or gamma-1 constant regions. In the humanized heavy chain,

CC amino acids H27, H28, H39, H30, H44 and H71 in the human HC VR

CC gensition of the mouse 21.6 Ig H Chain. Plasmids encoding the

CC chimeric antibodies are transfected into COS cells. The humanized

CC chimeric antibodies are transfected into COS cells. The humanized

CC antibodies can be used to inhibit adhesion of a leukocyte to an

CC endothelial cell and to treat inflammatory diseases such as multiple

CC clerosis. They can also be used in the treatment of stroke,

CC calso be used for detecting VLA-4, for affinity purification or for

CC also be used for detecting VLA-4, for affinity purification or for

CC generating anti-idiotype antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 11; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ99894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents the human reshaped antibody 21.6 heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                     AAW22428 standard; Protein; 142 AA
Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis;
                                                                   Humanised alpha-4 integrin antibody 21.6 VL version Ha
                                                                                                       09-DEC-1997
                                                                                                                                       AAW22428;
                                                                                                                                                                                                                                                                                           121 VSS 123
                                                                                                                                                                                                                                                         140 vss 142
                                                                                                                                                                                                                                                                                                                                                                                        80 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyamdywgqgtlvt 139
                                                                                                                                                                                                                                                                                                                                       61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 655; DB 16; 100.0%; Pred. No. 6.4e-53;
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CC This polypeptide, designated Ha, comprises the heavy chain variable CC region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also CC AAM22413). It is composed of complementarity determining regions from CC antibody 21.6 and a modified human 21/28 CL framework. It can be CC expressed in mammalian host cells following PCR amplification and CC expressed in mammalian host cells following PCR amplification and CC mutagenesis of appropriate mouse and human DNA sequences. The CC mutagenesis of appropriate mouse and human DNA sequences. The CC manufacture of a medicanent for treating asthma, atherosclerosis, CC manufacture of a medicanent for treating asthma, atherosclerosis, CC arthritis, transplant rejection, graft versus host disease, tumour CC antibody has a half-life in the human circulation essentially cc antibody has a half-life in the human circulation essentially antibody has a half-life in the human circulation essentially cc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bendig MM,
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/note- "21.6 complementarity determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "VH version Ha (Claim 25)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- Leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leger OJ, Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yednock TA;
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Best Local Similarity
WO9718838-A1.
                                            Region
                                                                              Region
                                                                                                                         Misc-difference
                                                                                                                                                             Region
                                                                                                                                                                                              Region
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                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                            /note= "21/28'CL framework region 1" Misc-difference 27..30
                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia;
                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                               Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                                                                       acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised alpha-4 integrin antibody 21.6 VH Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW22413 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 vss 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyamdywgqgtlvt 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
              /note= "21/28'CL framework region 4"
                                             /label- CDR3
/note- "21.6 complementarity determining region
                                                                                         /note= "21/28'CL Arg-72 is substd. by Ala of mouse 21.6 VL, important in supporting the CDR2
                                                                                                                                                            /note= "21.6 complementarity determining region 67..98
                               /label- FR4
                                                                                                                                                                                                                               /note= "21.6 complementarity determining region 36..49
                                                                                                                              /note= "21/28'CL framework region
                                                                                                                                                                                                  /note= "21/28'CL framework region
                                                                                                                                                                                                                                                                              /note= "21/28'CL residues 27-30 are replaced by those of MAD 21.6, involved in antigen
                                                                                                                                                  /label- FR3
                                                                                                                                                                                  /label- CDR2
                                                                                                                                                                                                                                                    /label= CDR1
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    /label- FR1
                                         ..123
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                                                                                      doot,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 655; DB 18;
Pred. No. 6.4e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 142;
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OS Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         composed of complementarity determining regions (CDRs) from the VH creation (see AAW22410) of mouse alpha-4 integrin monoclonal antibody creation (see AAW22410) of mouse alpha-4 integrin monoclonal antibody composed a modified human 21/28 CL framework. It can be expressed composed and a modified human 21/28 CL framework. It can be expressed composed co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This polypeptide, designated Ha, comprises the heavy chain variable region (VH) of a humanised alpha-4 integrin antibody 21.6. It is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; Fig 7; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of naturally occurring human antibodies.
                                                                                                                                                 Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
                                                                                                                                                                                                   02-APR-1996 (first entry)
                                                                                                                                                                                                                                                    AAR81330;
                                                                                                                                                                                                                                                                                                   AAR81330 standard; Protein; 123 AA
                            Mus musculus.
                                                                                                Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                           antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                             121 vss 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 98.9%;
Local Similarity 99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVOLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDDANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyandywgqgtivt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones ST, Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US18807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain curiable region (without signal sequence). Cloned cDNA CDR sequences of constant framework regions of the REI antibody for the light chain and constant framework regions of the REI antibody for the light chain and constant framework regions of the REI antibody for the light chain and condified using PCR primers (see AAQ9895-98) and then subcloned into combination cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, constant regions. In the humanized light chain, amino acids L45, L49, constant regions. In the humanized light chain, amino acids L45, L49, constant regions. In the humanized light chain, amino acids L45, L49, constant regions. In the humanized light chain, amino acids L45, L49, constant regions. In the humanized light chain, amino acids L45, L49, constant leaves and L69 in the humanized and toward are replaced by the amino constant present in the equivalent position of the mouse 21.6 Ig light cells and L69 in the humanized antibodies are transfected into COS chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a cultiple sclerosis. They can also be used in the treatment of stroke, carebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating constant purification or for generating constant purification or for generating vLA-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 68; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanised antibodies against VLA-4 - used for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukocyte adhesion to endothelial cells, partic.
Sequence
                                                            anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones TS,
         123 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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    region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50..66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "mouse heavy light chain variable framework
region 4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FR2
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Query Match

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The sequence represents the mouse antibody 21.6 heavy chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 102; Conserv
                                              Disclosure; Fig 2; 105pp; English.
                                                                        New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                N-PSDB; AAQ99892
                                                                                                                          WPI; 1995-269276/35.
                                                                                                                                                Bendig MM,
                                                                                                                                                                 (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                          25-JAN-1994;
                                                                      inflammatory disease.
                                                                                                                                                                                                              25-JAN-1995;
                                                                                                                                                                                                                                   27-JUL-1995
                                                                                                                                                                                                                                                       W09519790-A1.
                                                                                                                                                                                                                                                                                        Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse VLA-4 antibody 21.6 light heavy variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR81327 standard; Protein; 140 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTVIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                     94US-0186269.
                                                                                                                                                                                                           95WO-US01219.
                                                                                                                                                                                                                                                                                     /note-
132..1/
                                                                                                                                                                                                                                                                                                         118..131
                                                                                                                                                                                                                                                                                                                                                   /note= "framework region 2"
69..85
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55..68
                                                                                                                                                                                                                                                                      /note= "framework region 4"
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                                                                                                                                                                                                                                                                                                                                /note-_ *complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                  /note= "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                            Leger OJ,
                                                                                                                                                                                                                                                                                                               "framework region 3"
                                                                                                                                                                                                                                                                                        "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                          "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.7e-43;
1; Mismatches 10;
                                                                                                                                           Saldanha J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99965-98) and then subcloned into Constant regions. In the humanized heavy chain, amino acids H27, CC by the amino acid present in the human RC VR framework are replaced CC 21.6 Ig H chain. Plasmids encoding the chimeric antibodies are CC transfected into COS cells. The humanized antibodies can be used CC to inhibit adhesion of a leukocyte to an endothelial cell and CC can also be used in the treatment of stroke, cerebral traumas, CC detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 100;
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                                   Region
                                                                            Reg Lon
                                                                                                                                                                                                                                                                                           asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                     Region
                                                                                                                                                              Reg ion
                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                  Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                                                                                                                               Alpha-4 integrin mouse MAb 21.6 VH region.
                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW22410;
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/note= "framework region 3"
                                    /note= "complementarity determining region 2"
                  /label- FR3
                                                         /label- CDR2
                                                                                   /note= "framework region 2"
                                                                                                    /label- FR2
                                                                                                                      /note= "complementarity determining region 1"
                                                                                                                                             /label= cDR1
                                                                                                                                                                    /note= "framework region 1"
                                                                                                                                                                                        /label= FR1
                                                                                                                                                                                                                  /label= Leader
                                                                                                                                                                                                                                             Location/Qualifiers
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Complementarity determining regions (CDRs) of the 21.6 VH can be cincorporated into a human 21/28 CL framework to produce a claimed CC humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6 CC creating a disease selected from asthma, atherosclerosis, AIDS, CC treating a disease selected from asthma, atherosclerosis, AIDS, CC dementia, diabetes, inflammatory bowel disease, rhemmatoid cerhititis, transplant rejection, graft versus host disease, tumour CC eritaria, and acute leukocyte mediated lung injury. The antibody CC ischaemia, and acute leukocyte mediated lung injury. The antibody CC may also be used in the affinity purification of alpha-4 integrin CC for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibodies of the convention have a half-life in the human circulation essentially CC equivalent to that of naturally occurring human antibodies.
AAW44124
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AC AAW4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Page 69-70; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bendig MM, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This polypeptide comprises the heavy chain variable region (VH) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma, atherosclerosis, AIDS, dementia, etc.
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                                                                                                                                                                                                                                                                                                                  Sequence
 Heavy chain variable region of humanised NR-LU-13 antibody NRX451
                       05-JUN-1998 (first entry)
                                              AAW44124;
                                                                    AAW44124 standard; Protein; 120 AA.
                                                                                                                            140 v 140
                                                                                                                                                 121 V 121
                                                                                                                                                                    Local
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                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                               100;
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                                                                                                                                                                                                                                                                                                                      140 AA;
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/note= "complementarity determining region 3"
132..140
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                                                                                                                                                                                                                                                                          83.1%;
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                                                                                                                                                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                                                          Score 544; DB 18;
Pred. No. 1.1e-42;
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                                                                                                                                                                                                                                                                    10;
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                                                                                                                                                                                                                                                                                       Length 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A novel humanised Ab (hAb) binds the antigen bound by NR-LU-13. The hAb, specifically NRX451, or its conjugates can be used for the manufacture of a diagnostic or medicament for cancer diagnosis or treatment. The hAb has reduced immunogenicity and toxicity in humans, but retains the ability to bind the NR-LU-13 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised antibody binds same human cancer antigen as antibody NR-LU-13 - useful for pre-targeting methods, conventional antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NEOR-) NEORX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the heavy chain variable region of the humanised murine anti-human cancer antigen antibody (Ab) NR-LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy and immunodiagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
02-APR-2001
                                                                    AAB30693 standard; Protein; 431 AA.
                                   AAB30693;
                                                                                                                                                                   118
                                                                                                                                                                                                     121 VSS 123
                                                                                                                                                                                                                                        61 dlsfqgrvtitadtsintaymelsslrsddtavyycsrevl---tgtwsldywgqgtlvt 117
                                                                                                                                                                                                                                                                            61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                             1 gvglvgsgaevkkpgasvkvsckasgfnikdtymhwvrqapggglqwmgridpangntkc 60
                                                                                                                                                                                                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
 (first entry)
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99..109
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                                                                                                                                                                                                                                                                                                                                                                                                    8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Score 523.5; DB 1
Pred. No. 6.9e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 120;
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Best Local S
Matches 102
                                                                                                                                                                                                                                                                                                                                              and a cloning site for insertion of a second nucleic acid sequence checoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a first nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer, e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins in particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A fusion of single chain antibody/streptavidin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with cancer, e.g. adenocarcinomas \dot{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goshorn SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1999;
03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-2000; 2000WO-US15595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200075333-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptavidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-091213/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NEOR-) NEORX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptavidin; tumour cell; cancer; adenocarcinoma;
hematological malignancy; huNR-LU-10; EGP40; EPCAM
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 10; 100pp; English.
265
                                   121
                                                                    208
                                                                                                                                         148
                                                                                                       61
                                                                                                                                                        1 QVQLVQSGAEVKXPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                   qvqlvqsgaevkkpgasvkvsckasgfnlkdtymhwvrqapgqglqwmgridpangntks 207
                                   VSS 123
                                                               dlsfqgrvtitadtsintaymelsslrsddtavyycsrevl---tgtwsidywgqgtlvt 264
                                                                                                      DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                     431 AA;
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Graves SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0137900
99US-0168976
                                                                                                                                                                                                                                79.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schultz JE,
                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                Score 523.5; DB : Pred. No. 2.8e-40
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGP40; EPCAM
                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                   10;
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                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                 Length 431;
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AAR76681
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                    δÃ
                                         밁
                                                                                Matches 103;
                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR76681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      medulloblastoma; brain tumour; treatment; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR76681 standard; Protein; 136
                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; murine; chimeric antibody; HEF-RVL-M21g(gamma)1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human/murine chimeric antibody HEF-RVL-M21g(gamma)1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-1996
                                                                                                                                                                                                                                                                                                                                     19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                             AAQ94539 encodes AAR76681 the human/murine chimeric antibody HEF-RVL-M21g(gamma)1. The antibody is reactive with human medulio-blastoma (a brain tumour) cells. The chimeric antibody can be
                                                                                                                                                                                                                        antigenicity
                                                                                                                                                                                                                                 Reconstituted antibody against human medullo:blastoma cells -contains high proportion of human antibody origin and has low
                                                                                                                                                                                                                                                                N-PSDB; AAQ94539
                                                                                                                                                                                                                                                                                              Ohtomo T, Sato K,
                                                                                                                                                                                                                                                                                                                                                         19-OCT-1994;
                                                                                                                                  Sequence
                                                                                                                                                     used in the diagnosis and treatment of this disease.
                                                                                                                                                                                                     Claim 26; Page 94; 120pp; Japanese
                                                                                                                                                                                                                                                                          WPI: 1995-200347/26
                                                                                                                                                                                                                                                                                                               (CHUS ) CHUGAI SEIYAKU KK
20
                                                                                            Local
                                                             QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                        qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 79
                                                                                            Similarity
                                                                                                                                   136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                     93JP-0291078
                                                                                                                                                                                                                                                                                                                                                         94WO-JP01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label - CDR 2
87..118
                                                                                                                                                                                                                                                                                                                                                                                                                                                  119
                                                                                                                                                                                                                                                                                                                                                                                                                   /label= FR 4
                                                                                                                                                                                                                                                                                                                                                                                                                             /label= CDR 3
127..136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- CDR 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- FR 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label FR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= FR 2
                                                                                          79.8%;
                                                                                                                                                                                                                                                                                               Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                  4; Mismatches
                                                                                          Score 523; DB 16; Length 136; Pred. No. 8.8e-41;
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                                                                                   10;
                                                                                  Indels
                                                                                   6.
                                                                                   Gaps
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Best Local Similarity

Pred. No.

2

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RESULT 1
AAW04396
LD AAW04396
AW AAW04396
AW AAW04396
AW AAW04396
AW AAW0
AW MUTI
KW MUTI
KW Chim
KW C
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         Query Match
                                                                                                                                                                  human/murine light and heavy chain DNA mols. A recombinant vector for the expression of the heavy and light chain DNA mols. was prepd., and used to transform a host cell. The host cell was then cultured, and the expression prods. of the heavy and light chain DNA mols. sepd. and connected with a peptide linker to produce a single stranded FV region. The reshaped FV region has low human antigenicity, and is therefore expected to be useful as an agent for the diagnosis and treatment of cerebral tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                               monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAb, with human light and heavy
                                                                                          Sequence
                                                                                                                                                   e.g. myeloblastoma
                                                                                                                                                                                                                                                                                                                                                                                                    constant region sequences, respectively to produce chimaeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reshaped anti-human myeloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and treatment of cerebral tumours, e.g. myeloblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a fragment of the chimaeric human/murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHUS ) CHUGAI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-1994;
19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP08169900-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21-g(gamma)1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; treatment; cerebral tumour; reshaped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 vss 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 VSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1996-358509/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Pages 38-39; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT38653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123
                                                                                          136 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94JP-0252166.
93JP-0291078.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= CDR_2
118..125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= CDR_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label sig_peptide
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         79.88;
Score 523;
   DB 17;
   Length 136;
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RESULT
AAR76682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                           human antibody ONS-M21 Fv fragment. The plasmid was used in the construction of an expression vector, contg. cDNA encoding a human/murine chimeric antibody, reactive with human medulloblastoma (a brain tumour) cells. The chimeric antibody can be
                                                                                               Claim 35; Pages 98-99; 120pp; Japanese
                                                                                                                             Reconstituted antibody against human medullo:blastoma cells contains high proportion of human antibody origin and has lo
                                                                        AAQ94548 is the plasmid pSCFVT7-hM21, which encodes AAR76682 the
                                                                                                                                                                  N-PSDB; AAQ94548
                                                                                                                                                                            WPI; 1995-200347/26
                                                                                                                                                                                                   Ohtomo
                                                                                                                                                                                                                                            19-NOV-1993;
                                                                                                                                                                                                                      (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                  19-OCT-1994;
                                                                                                                                                                                                                                                                                        26-MAY-1995.
                                                                                                                                                                                                                                                                                                             WO9514041-A1
                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ONS-M21 antibody Fv fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR76682 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      medulloblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR76682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 vss 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 OVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn----qdywgqgttvt 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pSCFVT7-hM21; human; ONS-M21 antibody; chimeric blastoma; brain tumour; treatment; diagnosis; Fv
                                                                                                                                                                                                 Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity 83.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                            93JP-0291078
                                                                                                                                                                                                                                                                94WO-JP01763
                                                                                                                                                                                                                                                                                                                                /note= "FLAG"
                                                                                                                                                                                                                                                                                                                                                                 155..269
                                                                                                                                                                                                                                                                                                                                                                                       140..154
                                                                                                                                                                                                                                                                                                                                                                                                           /label* sig_peptide
23..139
                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     'note-
                                                                                                                                                                                                                                                                                                                                                                            /note-
                                                                                                                                                                                                 Tsuchiya
                                                                                                                                                                                                                                                                                                                                            . 269
                                                                                                                                                                                                                                                                                                                                                    "light variable region"
                                                                                                                                                                                                                                                                                                                                                                            "linker"
                                                                                                                                                                                                                                                                                                                                                                                              "heavy variable region"
                                                                                                                                                                                                 ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8e-41;
ches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                              has low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; fragment.
                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
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Sequence

in the diagnosis and treatment of this disease

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В
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The present sequence is a scFv fragment from the chimaeric human/murine monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAb, with human light and heavy constant region sequences, respectively to produce chimaeric for the expression of the heavy and light chain DNA mols. A recombinant vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                     Example 6; Pages 40-41; 45pp; Japanese.
                                                                                                                          treatment of cerebral tumours, e.g. myeloblastoma
                                                                                                                                     Reshaped anti-human myclobiastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and
                                                                                                                                                                                    N-PSDB; AAT38662.
                                                                                                                                                                                                                      (CHUS ) CHUGAI PHARM CO LTD
                                                                                                                                                                                                                                                18-OCT-1994;
19-NOV-1993;
                                                                                                                                                                                                                                                                                    18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                    JP08169900-A.
                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis; treatment; cerebral tumour; reshaped
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimaeric human/murine MAb ONS-M21 scFv fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW04397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW04397 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 vss 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn----qdywgqgttvt 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 qvq1vqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 82
                                                                                                                                                                                                1996-358509/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OVOLVOSGAEVKKPGASVKVSCKASGENIKDTYIHWVROAPGORLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                            94JP-0252166
93JP-0291078
                                                                                                                                                                                                                                                                                  94JP-0285057
                                                                                                                                                                                                                                                                                                                                                           /label= FLAG
                                                                                                                                                                                                                                                                                                                                                                                /note-
                                                                                                                                                                                                                                                                                                                                                                                                         /label- linker
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (label sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                               . 26
                                                                                                                                                                                                                                                                                                                                                                                                                                               .139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.8%;
83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                     .154
                                                                                                                                                                                                                                                                                                                                                                        269
                                                                                                                                                                                                                                                                                                                                                                                                                           "heavy variable region"
                                                                                                                                                                                                                                                                                                                                                                           light variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 523; DB 16;
Pred: No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caps
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8888888
              The sequence encodes the mouse antibody 21.6 heavy chain variable region, Hc, directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions are linked to human constant regions in the construction of a humanized modified using PCR primers (See AAQ99895-98) and then subcloned into constant regions. In the humanized human happa or gamma-1 constant regions. In the humanized light chain, amino acids L45, humanized ligh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
by the amino acid present in the equivalent position of the mouse
                                                                                                                                                                                                                                                                                               Claim 13; Page 70; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                             inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                            New humanised antibodies against VLA-4 - used for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bendig MM, Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09519790-A1
                                                                                                                                                                                                                                                                                                                                                                        eukocyte adhesion to endothelial cells, partic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUL-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanized VLA-4 antibody 21.6 heavy chain variable region, Hc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR81325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR81325 standard; Protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepd., and used to transform a host cell. The host cell was then cultured, and the expression prods. of the heavy and light chain DNA mols. sepd. and connected with a peptide linker to produce a single stranded FV region. The reshaped FV region has low human antigenicity, and is therefore expected to be useful as an agent for the diagnosis and treatment of cerebral tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 vss 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 dpkfqgrvtitadestntaymelssirsedtafyfca-sayyvn-----qdywgqgttvt 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DPKFOGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qvqlvqsgaevkkpgssvkvsckasgfnikdtylhwvrqapggglewmgridpadgntky 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0186269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US01219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.8%; Score 523; DB 17;
83.7%; Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6;
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RESULT 1
AAW22426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and for treating inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW22426 standard; Protein; 119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis;
                                                                                                                                                                                                                                                                                                                                                                                                               atopic dermatitis; psoriasis; myocardial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised alpha-4 integrin antibody 21.6 VH Hc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW22426;
                                                                                                                                                                                                                                                                                                                                                           Chimeric
                                                                                                                                                                                                                                                                                                                                                                      Chimeric Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                                                acute leukocyte mediated lung injury; therapy
                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                            Chimeric synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 vss 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 VSS 123
                                                                                                                                                                                                                                                          Misc-difference
                     /note= "21/28'CL framework region 3" Misc-difference 72
                                                                                                                                                        Region
                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DRKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 sqkfqgrvtitadtsastaymelsslrsedtavyycarggyfgs----gsnywgqgtlvt 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 gvqlvqsgaevkkpgasvkvsckasgfniksyamhwvrqapgqrlewmgwinagngntky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGFN1KDTY1HWVRQAPGQRLEWMGR1DPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 AA;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                             /note= "21/28'CL framework region 1" 27..30
                                                                                                                                                                                                                                            /note- *21/28'CL residues 27-30 are replaced by
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                       /note- "21.6 complementarity determining region 67..98
                                                                                                                                                                         /note-
 /note= "21/28'CL Arg-72 is substd. by Ala of 21.6 VL, important in supporting the
                                                                                                                             /note= "21/28'CL framework region
                                                                                                                                               /label= FR2
                                                                                                                                                                                      /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.6%;
82.9%;
                                                                                                                                                                         "21.6 complementarity determining region
                                                                                                                                                                                                                      binding"
                                                                                                                                                                                                                                 those of MAb 21.6, involved in antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 515; DB 16; Length 119; pred. No. 4.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
            mouse
CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
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XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                            An This polypeptide, designated HC, comprises the heavy chain variable CC region (VH) of a humanised alpha-4 integrin antibody 21.6. It is CC composed of complementarity determining regions (CDRs) from the VH CC region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody C2 1.6 and a modified human 21/28 CL framework. It contains an CC 21.6 and a modified human 21/28 CL framework. It contains an CC 21.6 VH version Ha (see AAW22412). Humanised CC claimed humanised 21.6 VH version Ha (see AAW22412). Humanised 21.6 CC 21.6 VH and VL regions are used to produce claimed humanised 21.6 CC antibodies useful in the manufacture of a medicament for treating CC asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory CC asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory CC asthma atherosclerosis, AIDS, dementia, diabetes, useful coversus host disease, tumour metastasis, nephritis atopic compatitis, psoriasis, myocardial ischaemia, and acute leukocyte compatitis, psoriasis, myocardial ischaemia, and acute leukocyte compatitis, psoriasis, myocardial ischaemia, and acute leukocyte compatitis, psoriasis, myocardial schaemia, and acute leukocyte compatitis, psoriasis, myocardial scha
                                                                                                                                     QΥ
                                                                                                                                                                                   В
                                     Qy
                                                                                          В
                                                                                                                                                                                                                                                                                Matches 102;
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9718838-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uses of humanised alpha-4 integrin antibody asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Fig 7; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
117 vss 119
                                          121 VSS 123
                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                     61 sqkfqgrvtitadtsastaymelsslrsedtavyycarggyfgs----gsnywgqgtlvt 116
                                                                                                                                     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                occurring human antibodies.
                                                                                                                    Jones ST, Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                       119 AA;
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0561521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113..123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- CDR3
/note- "21.6 complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99..112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "21/28'CL Tyr-102 is substd. by Phe of human VCAM-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "21/28'CL framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= FR4
                                                                                                                                                                                                                                                                                                            78.6%; Score 515; DB 18; 82.9%; Pred. No. 4.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   loop"
                                                                                                                                                                                                                                                                                          5.
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yednock TA;
                                                                                                                                                                                                                                                                                                                                          Length 119;
                                                                                                                                                                                                                                                                                                  Indels
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